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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic
25 intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

30 The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting
5 the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is
10 suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as
15 described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a
20 compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological
25 sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and
30 determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

5

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for

10 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN:

15 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous

20 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American

25 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM

30 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the

10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g.,

15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also

20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin

30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

5 "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

10 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
15 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
20 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

25 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
30 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP
5 program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

10 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than
15 about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a
20 polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

25 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site,
30 www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from
5 some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing
10 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally
15 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as
20 those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,
25 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter
30 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

- Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand
5 also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically
10 refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

15 A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids,
20 proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be
25 made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound
30 (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

5 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

10 As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage
15 other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with
20 isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid,
25 protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all.
30 By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times
5 background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For
10 high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high
15 stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy
20 permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar
25 stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly
30 or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these
15 light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild
20 conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant
25 DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies,
30 many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and
5 non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are
10 applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and
15 disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not
20 necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or
25 non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the
30 GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher
10 being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).

20 Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

25 Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access
30 to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or
5 absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.
10 Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued
15 and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval
20 system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S.
25 Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with
30 navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

- Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)
Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge
 University Press; Baxeavanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the
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- 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et
 al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and
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 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques
 Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps,
 Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and
 software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with
 15 data specifying the source of the target-containing sample from which each sequence specificity
 record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is
 from a control tissue sample known to be free of pathological disorders. In a variation, at least
 one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another
 20 tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate
 one or more of the following parameters for each target species in a sample: (1) a unique
 identification code, which can include, e.g., a target molecular structure and/or characteristic
 separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute
 and/or relative quantity of the target species present in the sample.

25 The invention also provides for the storage and retrieval of a collection of target data in
 a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-
 optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble
 memory devices, and other data storage devices, including CPU registers and on-CPU data
 storage arrays. Typically, the target data records are stored as a bit pattern in an array of
 30 magnetic domains on a magnetizable medium or as an array of charge states or transistor gate
 states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and
 a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method
5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount
10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed,
15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line,
20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a
30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

5 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can
10 be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal
15 comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

 The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be
20 stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different
25 samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the
30 smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase
10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In
15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH
20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.
30

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

5 In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature
10 provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained
15 sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in
20 screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid
25 operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

30 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-
5 bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-
10 positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable
15 markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using
20 techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida*
25 *albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer
30 protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other
5 components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-
10 cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of
15 purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription
20 or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than
25 about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

30 Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-
15 terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide
20 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol.
25 Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science
30 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, *supra*).

10 In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the
10 following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety. Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene
5 expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to,
10 quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene
15 expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as
20 being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays
25 are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can
30 be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or
5 heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

10 In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity,
15 creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques
20 Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired
25 characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical
30 library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FTTC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens
15 are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

10 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes
20 are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
25 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a
30 non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

5 In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

10 In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

15 Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface
25 of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular
30 manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

25 In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

- 5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.
- 10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

- In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
- 15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

- In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
- 20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

- 25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

- 30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

 In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

 In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

 In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or
5 immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the
10 endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the
15 chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) *Science* 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be
20 used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected
25 into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction
30 (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

5 In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) 15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as 20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and 25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, 30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by
5 conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be
10 selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be
15 about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

20 The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend
25 upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a
30 mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in
5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.
10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.
15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de
20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance
25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,
30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

5 In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

10 In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

15 It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

20 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

30 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynn, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs effected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiolomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodelling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented vitellodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskelatal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, cranioopharyngioma, pineoblastoma, pineocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma in situ, lobular carcinoma in situ
cervix: cancer of the cervix, vagina, or vulva
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastroduigestive carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
- 25 kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomyolipoma, oncocytoma
leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts, arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 30 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
- 35 ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, chorioncarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
- 40 prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumor, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- 45 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrosarcoma, smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskelatal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskelatal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotent mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, chorioncarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
- 60 uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenocarcinoma)

70 Tables 2B-72B, 76B, and 79B list accession numbers for Pkeys lacking Uniprot ID's for Tables 2A-72A, 76A, and 79A, respectively. For each probaset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-72C, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-72A, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymatrix Genechip arrays.

Pkey: Unique Eos probaset identifier number
ExAccn: Exemplar Accession number
UnigeneID: Unigene ID number

5	<p>Unigene Title: Unigene gene title</p> <p>Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), lei (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)</p> <p>Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)</p>
10	Pkey; ExAccn; UnigeneID; Unigene Title; Disease; Utility
15	<p>102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.</p> <p>104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member; angio; CTL</p> <p>104978; A1199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL</p> <p>109424; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.</p> <p>110765; AK000322; Hs.18457; hypothetical protein FLJ20316; colon, pros, stom, uter; mAb+diag</p> <p>110906; AA035211; Hs.17404; SOX7 SRY (sex determining) regl; angio, blad; CTL</p> <p>115622; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL</p> <p>116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL</p> <p>118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag</p> <p>123048; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag</p> <p>131486; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.</p> <p>133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag</p> <p>310016; AW449612; Hs.152475; ESTs; colon; CTL</p> <p>322303; A1357412; Hs.167601; ESTs; colon, pros, fibro, breast; CTL+diag</p> <p>400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.</p> <p>400297; A1127078; Hs.288381; hypothetical protein DKFZp5640; breast, blad, colon, pros; mAb</p> <p>400303; AA242758; Hs.78136; LIV-1 protein, estrogen regulat; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb</p> <p>400843; ; NM_003105; Homo sapiens sortil; blad; s.m.</p> <p>402075; ; ENSP00000251056; Plasma membra; blad, lung, headnk, cerv, mela, esoph; mAb+diag</p> <p>402801; ; NM_025206; Homo sapiens hypo; blad; CTL</p> <p>404287; ; FGENESH predicted novel CUB-do; panc, lung, colon, uter, esoph; mAb+s.m.</p> <p>404682; ; ortholog of mouse polydomain p; panc; diag</p> <p>404875; ; NM_022819; Homo sapiens phosph; blad; CTL+s.m.</p> <p>404977; ; Insulin-like growth factor 2 (s; blad, ovar, sarc; mAb+diag</p> <p>405033; ; C1002652; g154327; sp1Q04799; blad; s.m.</p> <p>408400; ; kallikrein 8 (neuropsin/ovastin; ovar, uter; diag</p> <p>406964; M21305; ; FGENESH predicted novel secret; angio, blad, fibro, sarc; diag</p> <p>407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE4299; glio, blad; CTL</p> <p>407792; A1077715; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag</p> <p>407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag</p> <p>407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member; angio; CTL</p> <p>407975; X89426; Hs.41718; endothelial cell-specific mole; angio, renal; diag</p> <p>408243; Y00787; Hs.624; interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag</p> <p>408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; mela; mAb+s.m.</p> <p>408369; R36438; Hs.118747; SLC15A2 Solute carrier family; pros, lung, fibro, uter, glio, cerv, ovar; mAb</p> <p>408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL</p> <p>408482; NM_000676; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m.</p> <p>408562; A1436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.</p> <p>408790; AW580227; Hs.47860; neurotrophic tyrosine kinase; lung; mAb+s.m.</p> <p>408908; BE288227; Hs.250822; serine/threonine kinase 16; blad, lung, headnk, stom, colon; s.m.</p> <p>409041; A0030325; Hs.50081; Hypothetical protein, XP_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag</p> <p>409079; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.</p> <p>409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL</p> <p>409178; BE393948; Hs.50815; kallikrein 5; ovar, breast, mela; diag</p> <p>409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.</p> <p>409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin (100k; lung, headnk, panc, stom, cerv, esoph, blad; diag</p> <p>409632; W74001; Hs.55278; serine (or cysteine) proteinase; lung, blad, headnk; diag</p> <p>409683; A1743750; Hs.95306; KIAA1882 protein; renal; CTL</p> <p>409757; NM_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag</p> <p>409889; AW630041; Hs.56937; suppression of tumorigenicity; colon, ovar, pros; mAb+s.m.</p> <p>409893; AW247090; Hs.57101; mitochondrion maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.</p> <p>409956; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag</p> <p>410001; A8041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung; diag</p> <p>410055; A1250839; Hs.58241; gene for serine/threonine prot; renal; s.m.</p> <p>410153; BE311828; Hs.15830; hypothetical protein FLJ12691; renal, blad; CTL</p> <p>410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL</p> <p>410308; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.</p> <p>410407; X68838; Hs.63287; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.</p> <p>410418; D31382; Hs.83325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.</p> <p>411274; NM_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag</p> <p>411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.</p> <p>411773; NM_006799; Hs.72026; protease, serine, 21 (fistulin; ovar; diag</p> <p>411975; A1818058; Hs.144583; 3'UTR of: dead ringer (Drosoph; test, colon; CTL</p> <p>412078; X69699; Hs.73149; paired box gene 8; ovar; CTL</p> <p>412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.</p> <p>412314; AA825247; Hs.356084; G protein-coupled receptor 27; ovar, uter, test; mAb+s.m.</p> <p>412609; Z48804; Hs.74124; ocular albinism 1 (Netherlands; mela; s.m.</p> <p>412628; A1972402; Hs.306051; hypothetical protein MGC2848; pros; diag</p> <p>412709; A1022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m.</p> <p>412718; AW016610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m.</p> <p>412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m.</p> <p>413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb</p>

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage); glio, ovar, blad, lung; diag
 413278; BE563086; Hs.833; interferon-stimulated protein; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela; CTL+s.m.
 413324; V00571; Hs.75294; corticotroph releasing hormon; blad; diag
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, mela, fibro, uter, sarc; s.m.
 413554; AA319146; Hs.75426; secretogranin II (chromogranin); panc, glio; diag
 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
 414555; N98589; Hs.76422; phospholipase A2, group IIA (p; pros; s.m.
 414577; A056548; Hs.378938; hypothetical protein FLJ20992; angio; CTL+diag
 414774; X02419; Hs.77274; plasminogen activator, urokin; lung, blad, headnk, panc, stom, ovar, esoph; diag
 414812; X72755; Hs.77367; monokine induced by gamma lnt; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mela, esoph; diag
 414883; AA926980; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
 414991; C17896; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
 415138; C18368; Hs.295944; tissue factor pathway inhibito; angio, panc, stom, lung, uter; CTL+diag
 415539; A1733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
 415668; AW957684; Hs.306814; Homo sapiens lysyl oxidase-lc; mela; diag
 415689; NM_005026; Hs.78589; serine (or cysteine) proteinase; lung; mAb+diag+s.m.
 415817; U89967; Hs.78867; protein tyrosine phosphatase; lung, glio, headnk, cerv, mela, esoph, fibro; mAb+s.m.
 416828; AA724373; Hs.304950; Homo sapiens mucopoln-3 (MCO3); mela; mAb
 416891; AF296370; Hs.283082; defensin, beta 3; headnk, esoph, mela; CTL+diag
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest decedent; lung, headnk, colon, uter, stom; CTL+s.m.
 416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); ovar, uter; diag
 416636; N32538; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mela; mAb+s.m.
 416658; U03272; Hs.79432; fibrillin 2 (congenital contra; lung, ovar, uter, blad, angio, test, sarc; diag
 416836; D54745; Hs.80247; cholecystokinin; pros, EWS, glio; diag
 416857; AA188775; Hs.292453; FGENSEH predicted TM containin; glio; mAb+s.m.
 416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
 417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
 417079; U65580; Hs.81134; interleukin 1 receptor antagon; blad, lung, headnk, cerv, esoph; diag
 417166; AA431323; Hs.42146; Paired box protein Pax-3; mela, sarc; CTL
 417389; BE260964; Hs.82045; milkline (neutite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon, sarc; mAb+diag
 417433; BE270268; Hs.82128; ST4 oncofetal trophoblast gly; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
 417771; AA804698; Hs.82547; retinolic acid receptor respon; blad, cerv, panc, pros, ovar; mAb
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
 417931; W95642; Hs.82961; trefol factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
 418007; M13508; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela; mAb+diag+s.m.
 418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag
 418064; BE387287; Hs.83384; S100 calcium-binding protein, ; mela; diag
 418281; U09550; Hs.1154; ovalductal glycoprotein 1, 120k; uter, ovar; CTL+diag
 418478; U98945; Hs.1174; cyclin-dependent kinase inhibito; lung, blad, ovar, headnk, panc, cerv, mela, sarc; s.m.
 418506; AA084248; Hs.372651; Unknown protein for MGC-29643; angio, ovar, glio, uter, lung, blad, panc, mela, sarc; mAb+diag
 418526; BE019020; Hs.85838; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.
 418678; NM_001327; Hs.87225; cancer-testis antigen (NY-ESO-1); lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
 418738; AW388633; Hs.8682; solute carrier family 7, (cali; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
 418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL
 418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.
 419080; AW150835; Hs.18876; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
 419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag
 419171; NM_002848; Hs.89655; protein tyrosine phosphatase, ; lung; mAb+s.m.
 419172; AW338825; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
 419183; U60859; Hs.89666; cytochrome P450, subfamily X04; blad, lung, headnk, panc; CTL+s.m.
 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
 419235; AW470411; Hs.288433; neurotrophin; panc, fibro, headnk, lung; mAb+diag
 419452; U33636; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-fam1; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
 419558; U29515; Hs.91093; chitinase 1 (chitinotriostase); lung, fibro, test; mAb+diag
 419704; AA428104; Hs.45057; ESTs; glio; CTL+s.m.
 419723; AL120183; Hs.338810; longevity assurance (LAG1, S. ; glio; mAb+diag
 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mela, sarc; CTL+s.m.
 419833; AA251131; Hs.220897; Homo sapiens typtophanyl-tRNA; fibro, stom, blad, esoph, uter; diag
 420159; A1572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad, stom; mAb
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, mela, sarc; s.m.
 420370; Y13645; Hs.97234; uropod 2; blad; mAb
 420440; NM_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag
 420602; AF060877; Hs.98236; regulator of G-protein signal; headnk, glio, cerv, mela; CTL+s.m.
 420610; A1683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
 420737; U08098; Hs.99898; CD70; tumor necrosis factor; renal; mAb+s.m.
 420876; AA918425; Hs.177744; FGENSEH predicted novel protein; panc, blad; s.m.
 421056; AU076725; Hs.101408; branched chain aminotransferase; blad, lung; CTL+s.m.
 421110; AJ250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
 421340; F07783; Hs.1369; decay accelerating factor for; angio, panc, stom; diag
 421378; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mela, esoph; diag
 421471; U90545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.
 421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.
 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
 421563; NM_006433; Hs.105806; granulysin; fibro; diag
 421574; AJ000152; Hs.105824; defensin, beta 2; headnk, lung; CTL+diag
 421582; A1910275; Hs.350470; trefol factor 1 (breast cance; breast, panc, lung, omuc; diag

- 421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-family; lung; mAb+s.m.
 421817; AF146074; Hs.108680; ATP-binding cassette, sub-family; lung, cerv, headnk, blad; mAb+s.m.
 421829; AB018330; Hs.108708; calcium/calmodulin-dependent g; pros; s.m.
 422046; NM_012445; Hs.288126; spondin 2, extracellular matrix; panc, pros, sarc; diag
 422083; NM_001141; Hs.111258; arachidonate 15-lipoxygenase; ; pros; s.m.
 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
 422192; AA305159; Hs.113019; fls485; mela; s.m.
 422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45); lung, blad, test, cerv, headnk, esoph; s.m.
 422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag
 422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ga; panc, stom, colon, esoph, renal, blad; CTL+s.m.
 422424; AJ186431; Hs.296638; prostate differentiation factor; blad, panc, pros, angio, colon, stom, lung, mela; diag
 422578; AF239666; Hs.1545; caudal type homeo box transcript; colon; CTL
 422577; BE336857; Hs.118787; transforming growth factor, bc; colon, renal, sarc; mAb+diag
 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
 422809; AK001379; Hs.121028; hypothetical protein FLJ10548; blad, cer, lung, uter, angio, stom, test; s.m.
 422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell; ovar, blad, panc, lung, headnk, colon, stom; CTL+s.m.
 423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
 423184; NM_004428; Hs.1624; ephrin-A1; pros, panc, renal, colon; mAb+s.m.
 423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL
 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
 423583; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 423634; AW959908; Hs.1690; heparin-binding growth factor; lung, blad, headnk, panc; diag
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
 423936; U77629; Hs.135639; achaete-scute complex (Drosoph; colon, stom, ovar; CTL
 423981; D13666; Hs.136348; perostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
 424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase; headnk, lung, cerv; diag
 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
 424381; AA285249; Hs.146328; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
 424411; NM_005209; Hs.146459; crystallin, beta A2; panc, sarc; s.m.
 424502; AF242388; Hs.149585; longsin; lung; s.m.
 424503; NM_002206; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
 424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ga; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
 424825; AF207069; Hs.153357; procollagen-lysine, 2-oxoglutar; mela; CTL+s.m.
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.
 424917; AL636208; Hs.96901; hypothetical protein FLJ23049; fibro, uter, ovar; CTL
 424943; AU077280; Hs.153924; death-associated protein kinase; fibro; s.m.
 425009; X58288; Hs.154151; protein tyrosine phosphatase; ; renal, fibro; mAb+s.m.
 425071; NM_013989; Hs.154424; delodnase, lodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
 425119; R44684; Hs.129958; downstream of. G protein-coupl; glio; mAb+s.m.
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
 425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
 425322; U83630; Hs.155637; protein kinase, DNA-activated; lung, headnk; s.m.
 425535; AB007937; Hs.158287; syndecan 3; mela, glio; mAb+s.m.
 425660; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb
 425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb
 425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
 425734; AF056209; Hs.159396; peptidylglycine alpha-amidat; lung; s.m.
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
 425842; AJ687490; Hs.159623; NK-2 (Drosophila) homolog B; panc, glio; s.m.
 425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.
 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
 425958; AU076628; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
 426028; NM_001110; Hs.172028; a disintegrin and metalloprote; blad; mAb+diag
 426215; AW983418; Hs.155223; stanniocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
 426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
 426322; J05068; Hs.2012; transcobalamin 1 (vitamin B12; panc, blad, stom; diag
 426344; J41821; Hs.322489; transcriptional activator of t; glio; CTL+s.m.
 426427; M86698; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
 426451; AJ908165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
 426514; BE816833; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag
 426600; NM_003378; Hs.171014; VGF nerve growth factor induc; mela, sarc; diag
 426761; AJ015709; Hs.172089; PORIMIN Pro-oncosis receptor 1; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
 426812; AF105365; Hs.172613; solute carrier family 12 (pot; renal; mAb+s.m.
 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
 427239; BE270447; Hs.356512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.
 427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL
 427343; AB880044; Hs.176977; protein kinase C binding prote; glio; CTL+s.m.
 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
 427923; AW274357; Hs.301406; FGENSEH predicted 11 TM protei; mela; mAb
 427969; NM_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag
 428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL
 428179; AJ127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
 428187; AJ687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
 428242; H55708; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

- 428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.
 428330; U22524; Hs.2258; matrix metalloproteinase 7 (mx; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
 428392; H10233; Hs.2265; secretory granule, neuroendoor; panc; diag
 5 428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.
 428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.
 428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag
 10 428505; AL035461; Hs.2281; chromogranin B (secretogranin; panc, lung; diag
 428513; BE220806; Hs.184697; plexin C1; mela, panc, breast stom, headnk; mAb
 428579; NM_005766; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter, mAb+s.m.
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.
 428698; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar, EWS; mAb
 15 428748; AW583206; Hs.98785; Ksp37 protein; lung, sarc; diag
 428758; AA433988; Hs.98502; CA125 antigen; nuon 16; ovar, cerv, lung, panc, stom, renal; diag
 428778; AK000530; Hs.193328; fibroblast growth factor recep; ovar; mAb+s.m.
 428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
 428969; AF120274; Hs.184689; artemin; lung, cerv; diag
 20 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.
 429149; AW193360; Hs.197982; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.
 429211; AF052693; Hs.198248; gap junction protein, beta 5 (j; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.
 25 429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros; mAb+s.m.
 429547; AW009168; Hs.98376; FGENESH predicted novel secret; panc, headnk, lung, ovar; diag
 429610; AB024937; Hs.211092; LUNX protein; FLUNC (palate lu; lung, fibro; mAb+diag
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin; lelo; mAb+s.m.
 30 430147; R60704; Hs.234434; hairyenhancer-of-split related; glio; s.m.
 430178; AW449612; Hs.152475; 3'UTR of: echaele-scute complex; colon, stom, ovar; CTL
 430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
 430413; AW842182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag
 430486; BE062108; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv, esoph; mAb+s.m.
 35 430822; AJ006371; Hs.248017; glyceraldehyde-3-phosphate dehy; mela, sarc; s.m.
 431130; NM_006103; Hs.2719; HE4; epikidymis-specific, whey; ovar, uter; diag
 431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag
 431515; NM_012152; Hs.258583; EDG-7 (endothelial different; ovar, pros, lung, blad; mAb+s.m.
 431620; AA126108; Hs.264881; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.
 40 431629; AU077025; Hs.265827; interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
 431630; NM_002204; Hs.266329; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadher; fibro, ovar, uter; mAb
 431840; AA534908; Hs.2880; POU domain, class 5, transcrip; test, renal, blad; CTL
 431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
 45 431858; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
 432101; A1918950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.
 432186; AW300888; Hs.273290; hypothetical protein FLJ10830; renal; CTL
 432201; AK538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung; mAb+diag+s.m.
 50 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL
 432596; AJ224741; Hs.278461; matrilin 3; panc, breast, sarc; diag
 432606; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
 432829; W60377; Hs.57772; ESTs; blad; CTL+s.m.
 432874; W94322; Hs.279551; melanoma inhibitory activity; panc, stom, mela, sarc; diag
 55 432890; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.
 433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag
 433848; AF085719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.
 433887; AK000596; Hs.3618; hippocalin-like 1; renal; CTL
 60 434205; AW136973; Hs.362915; ESTs, Weakly similar to 865890; colon, lung, stom; CTL+s.m.
 434276; AF123659; Hs.93605; leukine zipper, putative tumor; mela; s.m.
 434293; NM_004445; Hs.3796; EphB6; blad, pros; s.m.
 435013; H91923; Hs.110024; NM_020142; Homo sapiens NADHtub; renal, lung, sarc; CTL
 65 435472; AW972330; Hs.283022; triggering receptor expressed; glio; mAb
 435505; AF200492; Hs.211236; Interleukin-1 homolog 1; lung, headnk; diag
 436456; AW292677; Hs.248122; melanin-concentrating hormone; mela, glio; mAb+s.m.
 436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.
 436491; AA379597; Hs.6199; HSPC150 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; s.m.
 70 436576; A1458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.
 436606; AA628980; Hs.192371; down syndrome critical region; blad, lung, sarc; CTL+s.m.
 436895; AF037336; Hs.5338; carbonic anhydrase XII; breast, renal, ovar, glio; mAb+s.m.
 436961; AW376974; Hs.156704; ESTs; lung, panc, renal, uter, colon; CTL
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extrac; ovar, fibro; diag
 437016; AU076916; Hs.5398; guanine monophosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.
 75 437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
 437769; A1581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
 437852; BE001836; Hs.258897; putative GPCR; blad, lung; mAb+s.m.
 438380; T06430; Hs.6194; chondroin sulfate proteoglyc; glio, mela; diag
 438549; BE366601; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
 439018; AW300887; Hs.26838; membrane-spanning 4-domains, c; uter, stom, pros, fibro; mAb
 80 439223; AW238299; Hs.250518; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
 439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.
 439589; AW602168; Hs.222399; CEGP1 protein; breast, pros, blad; diag
 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

- 439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
 440006; AK000617; Hs.6844; NALP2 protein; PYRIN-Containing; blad, ovar, lung, headnk, test; s.m.
 440065; W03478; Hs.265331; Homo sapiens Fc receptor homod; mela; diag
 440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glio, ovar, uter, renal, hepC; mAb+diag
 440872; AF089811; Hs.7345; MAD1 (mitotic arrest deficient); mela; s.m.
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog; lung, blad, headnk, test, mela, esoph; s.m.
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane pr; ovar, uter; mAb
 442275; AW449467; Hs.54795; Homo sapiens secretoglobin, fa; fibro; diag
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; fibro, ovar, uter; CTL
 443105; X95753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
 443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
 443695; AF169312; Hs.9613; PPAR(gamma) angliopolein relat; renal; diag
 443648; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag
 443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
 443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
 444008; BE395095; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
 444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
 444371; X9540274; Hs.239; forkhead box M1; lung, headnk, blad, glio, test, mela; s.m.
 444391; BE387335; Hs.293713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag
 444486; AW192879; Hs.356660; ancient conserved domain prote; renal; mAb+s.m.
 444527; NM_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag
 444783; AK001408; Hs.62180; anillin (Drosophila Scapa hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.
 445417; AK001058; Hs.12680; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
 445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc, esoph; mAb
 445895; D29954; Hs.13421; KIAA0055 protein; pros; CTL
 446051; BE048061; Hs.37064; ephrin-A3; colon, breast; mAb+diag
 446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.
 446341; AJ040763; Hs.310735; FGENSEH prediction similar to ; mela; mAb+s.m.
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
 446921; AB012113; Hs.16530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag
 447033; AJ357412; Hs.157601; Predicted gene; Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag
 447072; D61594; Hs.17279; tyrosylprotein sulfotransferase; glio, panc; CTL+s.m.
 447131; NM_004585; Hs.17466; retinoic acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.
 447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag
 447269; NM_004861; Hs.17958; carbodiimide (3'-phosphoadenyly; renal; CTL
 447342; AJ199268; Hs.19322; Homo sapiens. Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
 448243; AW369771; Hs.367688; Integrin, beta 8; ovar, uter, lung, stom, headnk, glio, panc ; mAb+s.m.
 448610; NM_006157; Hs.21602; mel (chicken)-like 1; mela, sarc; diag
 448733; NM_005629; Hs.197958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
 448844; AI581519; Hs.177184; FGENSEH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
 449032; AA045573; Hs.22900; nuclear factor (erythroid-der; colon, test, stom; CTL+s.m.
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glio, headnk, lung, sarc; mAb
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
 449720; AA311162; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 449722; BE280074; Hs.23980; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.
 450001; NM_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.
 450375; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
 450701; H39950; Hs.288467; hypothetical protein XP_038151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag
 450726; AW204600; Hs.355462; HUMPSBPA Human pulmonary surf; fibro, lung; s.m.
 450831; N26168; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.
 450963; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag
 451310; AW250651; Hs.26213; Human DNA sequence from clone ; colon, panc; CTL
 451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb
 451537; R56631; Hs.26560; retinoid X receptor, gamma; mela; CTL+s.m.
 451668; Z43948; Hs.328444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag
 451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL
 451978; F08972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL
 452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag
 452180; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast, stom, panc; mAb
 452194; AI694413; Hs.373599; olfactory receptor, family 2 ; stom, panc, renal, colon, mela, fibro; mAb+s.m.
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast, headnk, panc, stom, lung, esoph, fibro; diag
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-I; blad, breast, panc, headnk, stom, lung, leuk, renal, esoph; diag
 452431; U88879; Hs.29498; toll-like receptor 3; renal, hepC; mAb
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIF; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb
 452838; U65011; Hs.30743; preferentially expressed antig; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL
 452862; AW378065; Hs.8887; ADAMTS2 (a disintegrin-like a; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
 453498; AA442103; Hs.33084; solute carrier family 2 (facil; renal, pros; mAb+s.m.

453837; AL138387; Hs.256126; baculoviral IAP repeat-contains; renal, mela, sarc; s.m.
 453968; AA847843; Hs.82711; High mobility group (nonhistone); lung, uter, blad, test; CTL+s.m.
 456546; AI690321; Hs.203845; KCNK15 potassium channel, subf. over; mAb+s.m.
 456662; NM_002448; Hs.1494; mesh (Drosophila) homeo box hom; uter, ovar; CTL
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma; panc; s.m.
 457489; AI893815; Hs.127179; cryptic gene; panc, pros, lung, diag
 457819; AA057484; Hs.35405; FLJ20522 Hypothetical protein; lung, cerv, headnk; mAb+diag
 458079; AJ796870; Hs.381220; Homo sapiens similar to RIKEN; mela, fibro, sarc; mAb
 458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

414991 1785136_1 D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122821,124019-12416
402901	8894222	Minus	175428-175667
404267	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9255298	Plus	1553-1712,1878-2140,4252-4385,5822-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2700 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number
 UnigenelD: Unigene ID number
 Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), ovum (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

100125; R02740; Hs.137656; putative chemokine receptor; G; blad; mAb+s.m.
 100131; D12485; Hs.11851; ectonucleotide pyrophosphatase; breast; mAb
 100147; D13668; Hs.136348; perlestin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag
 100241; BE273643; Hs.32983; cadherin 6, type 2, K-cadherin; blad; mAb
 100299; D49489; Hs.2177; growth differentiation factor; EWS; diag
 100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 100365; AI878827; Hs.79284; mesoderm specific transcript; colon, pros; diag
 100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.
 100405; AW291587; Hs.82733; nidogen 2; angio; diag
 100420; D88983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, angio, leuk; diag
 100448; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.
 100452; D87742; Hs.241552; KIAA0268 protein; pros; diag
 100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (c; lung; CTL+s.m.
 100654; A03756; Hs.184411; NM_000477; Homo sapiens albumin; pros; diag
 100655; A03758; Hs.184411; Empirically selected from AFFX; pros; diag
 100668; L05424; Hs.169610; CD44 antigen (homolog function); lung, breast; mAb
 100824; AI383237; Hs.193989; runt-related transcription fac; ovar; CTL+s.m.
 100930; J04129; Hs.82269; progesterone-associated endomet; lung; diag
 101063; D54745; Hs.80247; cholesterylolnlin; pros, EWS; diag
 101097; BE245303; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.
 101104; AW862258; Hs.169286; neuropeptide Y receptor Y1; breast, EWS; mAb
 101182; BE247295; Hs.78452; solute carrier family 20 (phos; angio; mAb+s.m.
 101193; L20861; Hs.152213; wingless-type MMTV integration; blad, lung; diag
 101249; L18964; Hs.1904; protein kinase C, lora; ovar; s.m.

- 101261; D30857; Hs.82353; protein C receptor, endothella; angio; mAb+s.m.
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA; pros; mAb+s.m.
 101431; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad; diag
 101447; M21305; ; gb:Human alpha satelite and s; angio, blad; diag
 101461; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; diag
 101485; AA296520; Hs.89548; selectin E (endothelial adhesi; pros, ovar; mAb
 101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb
 101526; NM_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb
 101543; M31166; Hs.2050; pentaxin-related gene, raplcty; angio, ovar; diag
 101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.
 101560; AW959272; Hs.347326; intercellular adhesion molecu; angio; mAb
 101626; M57399; Hs.44; pleiotrophin (heparin binding; lung; diag
 101649; AW959908; Hs.1690; heparin-binding growth factor; lung, blad; diag
 101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (c; breast, pros, blad, lung; mAb+CTL
 101741; NM_003199; Hs.326188; transcription factor 4; angio; CTL+s.m.
 101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb
 101759; M80244; Hs.184601; solute carrier family 7 (catio; lung, glo, blad, headnk; mAb+s.m.
 101791; M83822; Hs.82364; cell division cycle 4-like; pros; s.m.
 101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
 101809; M86849; Hs.323733; gap junction protein, beta 2; colon, blad, lung, panc, headnk; mAb
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gl; ovar, pros; mAb
 101845; U88674; Hs.78867; protein tyrosine phosphatase; lung, glo, headnk, cerv; mAb+s.m.
 101851; BE260964; Hs.82045; midkine (neurot growth-promot; lung, blad, ovar, breast, panc; mAb+diag
 102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.
 102012; BE259035; Hs.118400; singed (Drosophila)-like (sea; angio; diag
 102024; AA301887; Hs.76224; EGF-containing fibulin-like ec; angio; diag
 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
 102125; NM_008456; Hs.288215; sialyltransferase; breast, lung, ovar; s.m.
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 102154; U17760; Hs.75517; laminin, beta 3 (niceln (125kD; lung, blad, headnk; diag
 102178; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag
 102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag
 102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.
 102208; U22961; Hs.184411; gb:Human mRNA clone with siml; pros; diag
 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
 102297; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 102304; AF015224; Hs.46452; mammaglobin 1; breast; diag
 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad; diag
 102348; U37519; Hs.87539; aldehyde dehydrogenase 3 famil; lung, blad; s.m.
 102380; U40434; Hs.156981; mesothelin; ovar; diag
 102394; NM_003816; Hs.2442; a disintegrin and metalloprote; panc; s.m.
 102455; U48705; Hs.75582; discoidin domain receptor fam; breast; mAb
 102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
 102522; BE250944; Hs.183556; solute carrier family 1 (neut; pros; mAb
 102581; AU077228; Hs.77258; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.
 102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL
 102623; AW249285; Hs.37110; melanoma antigen, family A, S; lung, blad; mAb+CTL
 102668; U71207; Hs.29279; eyes absent (Drosophila) homot; lung, pros; CTL+s.m.
 102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.
 102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb
 102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar; diag
 102745; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 102803; H48299; Hs.26126; claudin 10; ovar; mAb
 102829; NM_006183; Hs.80962; neurensin; lung, ovar, headnk; diag
 102836; U34320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
 102852; Y00571; Hs.75294; corticotropin releasing hormon; blad; diag
 102898; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.
 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
 102917; AI016712; Hs.287797; Integrin, beta 1 (fibronectin; angio; mAb
 102927; BE512730; Hs.85114; keratin 18; ovar; diag
 102958; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 103003; AI910275; Hs.350470; bcl-2 factor 1 (breast cancer; breast, panc; diag
 103021; BE001596; Hs.85266; Integrin, beta 4; lung blad; mAb
 103038; M13508; Hs.83169; matrix metalloproteinase 1 (inc; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.
 103037; BE018302; Hs.2894; placental growth factor, vascul; angio; diag
 103060; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.
 103080; AU077231; Hs.82932; cyclin D1 (PRAD1; parathyroid; breast, EWS; diag
 103085; NM_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb
 103111; NM_006103; Hs.2719; epididymis-specific, whey-acid; ovar, uter; diag
 103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
 103206; X72755; Hs.77367; monokine induced by gamma inte; breast, lung; diag
 103210; X72925; Hs.69752; desmocollin 1; pros; mAb
 103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin; angio, fibro; mAb+s.m.
 103298; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.
 103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb
 103365; X90908; Hs.74126; fatty acid binding protein 6; blad; diag

- 103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag
 103587; BE270265; Hs.82128; 5T4 oncofetal trophoblast glyco; breast, lung; mAb
 103594; AI368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.
 103682; AW137912; Hs.227583; Homo sapiens chromosome X map; angio; mAb+s.m.
 103739; AA115173; ; gb:zn30402.s1 Stratagene neuro; pros; s.m.
 103787; BE244657; Hs.348998; C9orf100 protein; angio; diag
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag
 104052; NM_002407; Hs.97644; mammaglobin 2; ovar; diag
 104115; AF183810; Hs.26102; opposite strand of: bichorh; breast; mAb
 104252; AF002246; Hs.210863; cell adhesion molecule with tr; ovar; diag
 104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag
 104308; N25117; Hs.355957; ribosomal protein S26; pros; diag
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 f; colon; diag
 104542; R29857; ; gb:F1-1179D 22 week old human; pros; diag
 104608; AF143857; Hs.337588; ESTs, Moderately similar to S6; blad; mAb
 104659; AW969769; Hs.100343; ESTs; EWS; diag
 104860; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb
 104867; AI239823; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag
 104889; AA420450; Hs.380068; Plakophilin; lung; diag
 104891; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
 104764; AI039243; Hs.278586; ESTs; angio; diag
 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
 104877; AI136633; Hs.22968; intron of VEGFR; renal; diag
 104888; AWS39591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, mAb+s.m.
 104919; AA026880; Hs.26252; Homo sapiens cDNA FLJ13603 f; breast, cerv, uter, mAb+s.m.
 104943; AF072873; Hs.114218; fizzled (Drosophila) homolog; ovar; mAb+s.m.
 104954; AW250851; Hs.26213; Human DNA sequence from clone; colon; diag
 104971; BE311926; Hs.15830; hypothetical protein FLJ12681; blad; CTL
 105012; AF096158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
 105039; AA907305; Hs.36475; ESTs; breast; diag
 105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 f; pros; diag
 105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
 105263; AW388633; Hs.6682; solute carrier family 7, (cat); angio, lung, ovar, blad, panc; mAb+s.m.
 105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag
 105301; AW352367; Hs.7457; MAGE1 protein; EWS; diag
 105316; AI671245; Hs.24835; hypothetical protein FLJ14504; EWS; mAb
 105329; AA234581; Hs.22862; ESTs; breast, pros; CTL+s.m.
 105330; AW338628; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 105370; AF178274; Hs.22791; transmembrane protein with EGF; pros; mAb+s.m.
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
 105503; AW953624; Hs.31707; ESTs, Weakly similar to YEWA_Y; pros, breast, colon; CTL+s.m.
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
 105516; AK001268; Hs.30738; hypothetical protein FLJ10407; ovar; diag
 105564; BE616894; Hs.288042; hypothetical protein FLJ14299; breast; diag
 105645; AW294631; Hs.351270; ESTs; pros; diag
 105715; BE621800; Hs.29444; putative small membrane protel; colon; diag
 105743; BE248502; Hs.9598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.
 105746; AW151952; Hs.48679; hypothetical protein FLJ20739; breast; CTL+s.m.
 105777; R42766; Hs.23066; ESTs; breast; diag
 105782; H09748; Hs.57987; B-cell CLL/lymphoma 11B (zinc); EWS; CTL+s.m.
 105828; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
 105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
 106000; AW194428; Hs.20728; ESTs; breast; diag
 106012; AI240665; Hs.352537; ESTs; breast, lung; diag
 106014; AF123094; Hs.180586; mucosa associated lymphoid tis; leuk; diag
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
 106066; AW274357; Hs.301406; hypothetical protein PP3501; mela; CTL+s.m.
 106111; AW075398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.
 106124; H93368; Hs.7587; branched chain aminotransferase; angio; s.m.
 106155; AA425414; Hs.33267; nuclear factor YB; breast, pros, angio; diag
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 f; colon; diag
 106414; BE568205; Hs.28827; mitogen-activated protein kina; breast; s.m.
 106448; Z42061; Hs.27004; ESTs; pros; diag
 106533; AL134708; Hs.145998; ESTs; EWS; diag
 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
 106579; AA456135; Hs.23023; ESTs; pros; diag
 106632; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 f; ovar; diag
 106793; H94997; Hs.16450; ESTs; angio; diag
 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
 106906; AA861271; Hs.222024; transcription factor BMAL2; lung, blad; diag
 106980; AA280722; Hs.24758; ESTs, Weakly similar to I3B022; breast; diag
 107038; AI973016; Hs.15725; hypothetical protein SBB148; pros; diag
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
 107105; AW963419; Hs.155223; stanniocalcin 2; breast; diag
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
 107151; AW378065; Hs.8887; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, lung, blad; mAb+diag
 107216; D51069; Hs.211579; melanoma cell adhesion molecul; angio; diag

- 107248; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.
 107284; NM_005529; Hs.187958; solute carrier family 6 (neuro; lung; mAb+s.m.
 107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
 107901; LA2612; Hs.335952; keratin 6B; breast, blad, lung; diag
 5 107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
 108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 fl; ovar; CTL+s.m.
 108153; AW619204; Hs.40808; ESTs; pros; diag
 10 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 108242; AA062746; Hs.355244; gbzm03g12.s1 Stratagene come; pros; diag
 108282; AA065142; gbzm03h11.r1 Stratagene fibro; pros; diag
 108505; AA083376; gbzm03g08.s1 Stratagene hNT r; pros; diag
 15 108679; AA115963; Hs.323423; ESTs, Moderately similar to B; pros; diag
 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
 108732; AA258888; Hs.107476; ATP synthase, H⁺ transporting; pros; s.m.
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
 108828; AK001693; Hs.273344; DKFZP564O043 protein; breast; diag
 20 108860; AA133334; Hs.816; ESTs; lung; s.m.
 109001; AJ056548; Hs.72116; hypothetical protein FLJ20992; angio; CTL+diag
 109032; AI219207; Hs.72222; hypothetical protein FLJ13458; blad; CTL
 109077; AI732617; Hs.182362; ESTs; blad; diag
 109112; AW419195; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 25 109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
 109166; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk; EWS; s.m.
 109220; AW958181; Hs.189998; ESTs; pros; diag
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
 109292; AW975746; Hs.188662; KIAA1702 protein; breast; diag
 30 109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag
 109456; AW958580; Hs.42689; ESTs; angio, panc; diag
 109614; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast; diag
 109630; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.
 109648; H17800; Hs.7154; ESTs; ovar; diag
 35 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
 110009; BE075297; Hs.6814; ESTs, Weakly similar to A43832; breast, colon; diag
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros; EWS; diag
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 110240; AI668594; Hs.176588; ESTs, Weakly similar to CP4Y_H; breast; diag
 40 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
 110675; H89365; Hs.249159; adrenergic, alpha-2A-, recepto; pros; mAb+s.m.
 110728; AA737108; Hs.32250; ESTs, Moderately similar to D; EWS; s.m.
 110844; AI740792; Hs.167531; methylcrotonyl-Coenzyme A car; pros, pros; s.m.
 110919; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
 45 110971; AI780098; Hs.21411; ESTs; pros; diag
 111157; AL109728; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 111179; AK000136; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.
 111185; AJ245871; Hs.12844; EGF-like domain, multiple 6; ovar, blad; mAb+diag
 111223; AA852773; Hs.334838; KIAA1868 protein; breast, colon, lung, EWS; mAb
 50 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
 111367; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag
 111384; N94608; Hs.288969; HSCARG protein; breast; diag
 111900; AF131784; Hs.25318; Homo sapiens clone 25184 mRNA; breast; diag
 111928; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 112134; R41823; Hs.7413; ESTs; calyculin-2; breast, EWS; diag
 55 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty; breast; s.m.
 112283; L14561; Hs.20952; ATPase, Ca⁺⁺ transporting, pla; ovar; mAb
 112287; AB033064; Hs.236453; KIAA1238 protein; breast; diag
 60 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
 113003; AW282315; Hs.7215; ESTs; EWS; diag
 113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 113047; AI571940; Hs.7549; ESTs; breast, colon; diag
 113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
 65 113188; AW002393; Hs.337629; gb:wu61d05.x1 NCL CGAP_G06 Hom; ovar; diag
 113195; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
 113230; T61430; gb:yc06a03.s1 Stratagene lung; blad; diag
 113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 113374; T79925; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
 70 113443; AW083820; Hs.16098; claudin 2; colon, panc; mAb
 113471; AI765890; Hs.16341; MAWD binding protein; pros; diag
 113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 fls; colon; diag
 113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros; diag
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 75 114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag
 114251; H15251; Hs.21948; ESTs; breast; diag
 114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
 114452; AI369275; Hs.243010; Homo sapiens cDNA FLJ14445 fls; angio; diag
 80 114480; BE065778; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 114540; AI904232; Hs.75323; prohibitin; breast; diag
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus t; breast, pros; diag

- 114587; AF086009; Hs.298398; gbl:Homo sapiens full length in; colon; diag
 114724; R64730.comp; Hs.155986; DEADH (Asp-Glu-Ala-Asp/His) b; ovar; CTL+s.m.
 114768; AF212848; Hs.182339; ets homologous factor; pros; breast; colon; CTL+s.m.
 114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
 5 114908; AA454988; Hs.54973; cadherin-E6 protein VR20; pros; diag
 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
 114965; A1733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb
 115060; AF052693; Hs.198249; gap junction protein, beta 5 f; lung; blad; headnk; mAb+s.m.
 10 115221; AW365434; Hs.79741; hypothetical protein FLJ10118; ovar; diag
 115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag
 115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar; lung; CTL+s.m.
 115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag
 115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar; lung; blad; headnk; panc; cerv; stom; uter; colon; CTL+s.m.
 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
 15 115675; W87707; Hs.82065; interleukin 6 signal transducer; breast; pros; mAb+s.m.
 115683; AF255910; Hs.64650; junctional adhesion molecule 2; angio; glio; mAb
 115697; D31382; Hs.83325; transmembrane protease, serine; colon; blad; lung; ovar; panc; headnk; mAb+diag+s.m.
 115719; AW992405; Hs.352408; Homo sapiens, clone IMAGE:3507; pros; breast; colon; CTL+s.m.
 20 115819; AA486820; Hs.41135; endomucin-2; angio; diag
 115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag
 115844; AJ373052; Hs.332838; hypothetical protein MGC5370; pros; diag
 115881; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; EWS; uter; mAb+s.m.
 115892; AA291377; Hs.60831; ESTs; ovar; blad; lung; diag
 25 115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar; lung; diag
 115947; R47479; Hs.94761; KIAA1691 protein; colon; diag
 115978; AL035864; Hs.69517; cDNA for differentially expres; lung; blad; breast; pros; ovar; headnk; CTL
 116003; BE275469; Hs.66493; Down syndrome critical region; colon; mAb
 116011; AL358053; Hs.57664; Homo sapiens mRNA full length; breast; diag
 30 116028; H59799; Hs.42644; thiodioxin-like; ovar; lung; diag
 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung; breast; diag
 116202; BE159395; Hs.294092; ESTs; pros; diag
 116238; AV680717; Hs.47144; DKFZP586N0819 protein; ovar; diag
 116301; AW969706; Hs.293332; ESTs; EWS; diag
 35 116334; AL038450; Hs.48948; ESTs; pros; diag
 116335; AK001100; Hs.41690; desmocollin 3; lung; blad; headnk; diag
 116393; AI972402; Hs.306051; hypothetical protein MGC2848; pros; diag
 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
 116401; AW893940; Hs.59898; ESTs; ovar; diag
 40 116416; AW753876; Hs.39982; ESTs; ovar; diag
 116470; AI272141; Hs.351928; SRY (sex determining region Y); colon; breast; angio; blad; diag
 116483; AI346201; Hs.76118; ubiquitin carboxyl-terminal est; angio; lung; s.m.
 116610; D80448; Hs.184841; ESTs; pros; diag
 116732; AW152225; Hs.165909; ESTs, Weakly similar to I38022; colon; diag
 45 116787; AW362955; Hs.355547; Homo sapiens cDNA FLJ14415 fis; pros; breast; colon; pros; mAb
 116962; H79877; ; gbyu78g10.s1 Soares fetal liv; pros; diag
 117027; AW085208; Hs.130093; ESTs; breast; diag
 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; breast; colon; pros; diag
 117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
 50 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate lc; lung; mAb+diag
 117367; AI041793; Hs.42502; ESTs; breast; diag
 117412; N32536; Hs.42645; solida carrier family 18 (mono; breast; ovar; mAb+s.m.
 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk; diag
 55 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
 117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros; diag
 117984; AF189723; Hs.106778; ATPase, Ca++ transport; typ; pros; breast; colon; mAb
 118049; N53145; ; gbyu55X09.s1 Soares fetal liv; pros; diag
 118314; N48580; Hs.46692; ESTs; blad; lung; diag
 60 118336; BE327311; Hs.47166; HT021; breast; ovar; blad; pros; CTL+s.m.
 118368; N64339; Hs.48958; gap junction protein, beta 6 f; lung; blad; mAb
 118417; AF080229; ; gbl:Human endogenous retrovirus; pros; s.m.
 118472; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 118511; N75620; Hs.43157; ESTs; angio; diag
 65 118901; AW292577; Hs.94445; ESTs; breast; diag
 118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 119018; AA631143; Hs.278695; Homo sapiens protein mRNA, co; pros; pros; diag
 119036; R95872; Hs.117572; chemokine binding protein 2; breast; ovar; mAb
 119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio; pros; CTL+s.m.
 70 119082; AF252297; Hs.91646; cytochrome P450 retinoid metab; EWS; diag
 119128; R45175; Hs.117183; ESTs; pros; breast; colon; diag
 119279; N57668; Hs.48028; EST; breast; diag
 119307; BE048061; Hs.37054; ephrin-A3; colon; breast; mAb+diag
 119478; AI624342; Hs.179082; ESTs; breast; diag
 75 119617; AA518531; Hs.55999; NK homeobox (Drosophila), fam1; pros; diag
 119743; AA947552; Hs.68088; branched chain aminotransferase; ovar; s.m.
 119771; AI905687; Hs.348418; AI905687:IL-BT095-190199-019 B; breast; diag
 119780; NM_016625; Hs.191381; hypothetical protein; ovar; lung; CTL+s.m.
 119789; BE393946; Hs.50915; kallikrein 5; ovar; diag
 119845; W79129; Hs.58561; G protein-coupled receptor 87; lung; blad; headnk; cerv; mAb+s.m.
 80 119940; AL050097; Hs.272531; DKFZP586N0319 protein; pros; diag
 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon; lung; diag
 120132; W57554; Hs.125019; lymphoid nuclear protein (LAF; pros; breast; diag
 120147; AI917116; Hs.348941; hemoglobin, beta; EWS; diag

- 120206; H26735; Hs.91868; Homo sapiens clone PP1498 unkn; breast; mAb
 120242; AW969587; Hs.86366; ESTs; blad; diag
 120328; AA923278; Hs.290905; ESTs, Weakly similar to protea; pros; s.m.
 120438; AW015242; Hs.99468; ESTs, Weakly similar to YK54_Y; ovar; diag
 120471; AA251944; Hs.104058; CGI-29 protein; colon; diag
 120486; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk; diag
 120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 120824; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.
 120830; AI568170; Hs.98886; ESTs; EWS; diag
 120977; AA398155; Hs.97600; ESTs; breast, ovar; diag
 121027; AI572490; Hs.99785; Homo sapiens cDNA; FLJ21245 f; blad; mAb
 121231; AA814948; Hs.95343; ESTs, Weakly similar to ALUC_H; EWS; diag
 121335; AA404418; ; gb:zw37e02.s1 Scores_total_fet; angio; diag
 121362; AF060147; Hs.97932; chondromodulin I precursor; EWS; mAb
 121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag
 121619; AA528339; Hs.178052; ESTs, Weakly similar to phosph; EWS; s.m.
 121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag
 121721; AL047051; Hs.199981; ESTs, Weakly similar to ALU7_H; pros; diag
 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
 121748; BE538911; Hs.234545; hypothetical protein NUF2R; breast; diag
 121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar; mAb+CTL
 121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 121913; AI249368; Hs.98558; ESTs; protease inhibitor 15 f; breast, pros; s.m.
 121920; AA428300; ; gb:zw18e02.s1 Scores_ovary_lun; ovar, uter, cerv; diag
 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag
 122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB; breast; diag
 122802; AI887303; Hs.285529; G protein-coupled receptor 48; ovar, uter; mAb+s.m.
 122869; AW821262; Hs.104336; hypothetical protein; ovar; diag
 123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.
 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc; lung; diag
 123137; AJ073913; Hs.100688; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
 123158; AF161426; Hs.218328; hypothetical protein; breast; diag
 123160; AA488687; Hs.284235; ESTs, Weakly similar to I38022; lung; diag
 123169; AI950087; Hs.369628; gb:wg05c02.x1 NCL_CGAP_Kid12 H; ovar; diag
 123209; AW986543; Hs.203270; ESTs, Weakly similar to ALU1_H; pros; diag
 123308; C14187; Hs.157208; ESTs; EWS; diag
 123339; AW188464; Hs.101515; ESTs; ovar; diag
 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
 123494; AW179019; Hs.112110; mitochondrial ribosomal prot; ovar; diag
 123520; AA608550; ; gb:ae53d12.s1 Stratagene lung; pros; s.m.
 123533; AA808751; ; gb:ae56h07.s1 Stratagene lung; colon; diag
 123619; AA602954; Hs.366318; gb:nc097c02.s1 NCL_CGAP_Py2 Hom; breast; CTL+s.m.
 123688; AA399323; Hs.285130; Homo sapiens pinch-2 protein nt; ovar; diag
 123709; AA708910; Hs.112742; ESTs; breast; diag
 123828; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
 123972; T46848; Hs.70337; immunoglobulin superfamily, ma; ovar; diag
 124000; AI147155; Hs.279727; ESTs; homologues of PEM-3 (Cion; breast, angio, lung, ovar, EWS; diag
 124058; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
 124153; AJ077333; Hs.180483; erythrocyte membrane protein b; pros; mAb
 124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag
 124526; N62098; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.
 124579; AI693815; Hs.127179; cryptic gene; panc; diag
 124777; R41935; Hs.140237; ESTs, Weakly similar to ALU1_H; pros, breast; diag
 125103; AA570068; Hs.122730; ESTs, Moderately similar to K; colon; mAb
 125154; W38419; ; gb:zc78a07.s1 Pancreatic islet; ovar; diag
 125250; W26524; Hs.356686; protein phosphatase 4 regulator; ovar; CTL+s.m.
 125266; W90022; Hs.186809; ESTs, Highly similar to LCT2_H; angio; diag
 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
 125668; AL390172; Hs.317432; Homo sapiens cDNA; FLJ21270 f; ovar; diag
 125770; AA143045; Hs.81668; v-kit Hardy-Zuckerman 4 feline; EWS; diag
 125976; AA436760; Hs.35552; gb:zv67d11.r1 Scores_total_fet; pros; diag
 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 126545; AA316181; Hs.61636; six transmembrane epithelial tr; pros, breast, lung, panc, headnk, EWS; mAb+CTL
 126768; AI559444; Hs.104679; ESTs; pros, breast; mAb
 126799; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 126872; AW450979; ; gb:UJ-H-B13-ale-a-12-0-UJ.s1 N; blad; diag
 126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag
 126960; AL390172; Hs.317432; branched chain aminotransferase; ovar; s.m.
 126968; R38438; Hs.118747; solute carrier family 15 (H+); pros; mAb
 127093; AW816516; Hs.173540; ATPase, Class V, type 10D; pros; mAb
 127221; BE062109; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv; mAb+s.m.
 127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.
 127425; AF183810; Hs.26102; trichorhinophalangect syndrome; breast; mAb
 127478; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag
 127537; AI926047; Hs.162859; ESTs; pros; diag
 127664; AA806164; Hs.116502; ESTs; EWS; diag
 128046; AA873285; Hs.357313; gb:oh68h05.s1 NCL_CGAP_Kid5 Ho; pros, breast, colon; diag
 128305; AI954568; Hs.365708; matrix Gla protein; breast; diag
 128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.
 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

- 128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
 128734; AB008390; Hs.104570; kallikrein 8 (neuropsin/ovasin; ovar; diag
 128790; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, test, panc; diag
 128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS, leuk; diag
 128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
 128925; R67415; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag
 128948; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
 128959; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, cont; pros; diag
 129041; BE382756; Hs.169302; solute carrier family 2 (faci; lung, blad; mAb+s.m.
 129097; BE243933; Hs.108642; zinc finger protein 22 (KIX 15; ovar; CTL+s.m.
 129099; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, blad, headnk; mAb+s.m.
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 129260; AF077200; Hs.279813; hypothetical protein; colon; diag
 129284; AA318224; Hs.296141; ESTs; colon; diag
 129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA; breast; diag
 129389; NM_012445; Hs.268126; spondin 2, extracellular mab; colon, pros; diag
 129404; AI267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
 129466; I42693; Hs.334309; keratin 6A; lung, blad; diag
 129482; AA188185; Hs.269043; spindlin; breast; diag
 129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag
 129620; D75338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag
 129628; U36945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk s.m.
 129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 129689; AW748482; Hs.77873; B7 homolog 3; breast; diag
 129703; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
 129869; AJ222069; Hs.13015; hypothetical protein similar t; breast; diag
 129912; AF156086; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
 129953; AA412195; Hs.13740; ESTs; breast; diag
 129977; NM_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.
 130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag
 130057; AF027153; Hs.324787; solute carrier family 5 (inosi; breast; mAb
 130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 130181; AF052119; Hs.151608; Homo sapiens clone 23622 mRNA; pros; diag
 130184; H58306; Hs.15166; retinoic acid induced 14; angio; diag
 130262; D53216; Hs.153884; frizzled-related protein; panc, EWS, stom, renal; diag
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
 130385; AW067800; Hs.155223; stanniocalcin 2; breast, lung; mAb+diag
 130455; D90041; Hs.156866; N-acetyltransferase 1 (arylani; breast; s.m.
 130511; L32137; Hs.15684; cartilage oligomeric matrix pr; breast, ovar; diag
 130558; BE584937; Hs.15984; pp21 homolog; pros; CTL+s.m.
 130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag
 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
 130637; AA358764; Hs.17109; integral membrane protein 2A; EWS; mAb+s.m.
 130648; AI458165; Hs.17286; hypothetical protein MGC2376; colon; diag
 130667; BE248961; Hs.17539; Homo sapiens ubiquitin protein; breast; s.m.
 130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag
 130714; AJ348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
 130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 130800; AI187292; Hs.19574; hypothetical protein MGC5468; colon, lung; diag
 130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag
 130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.
 130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 130967; AA383071; Hs.182579; leucine aminopeptidase; ovar; s.m.
 130972; D81866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 130987; BE013289; Hs.21893; hypothetical protein DKFZp761N; colon; diag
 131046; AA321648; Hs.2246; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag
 131080; NM_001955; Hs.2271; endothelin 1; angio; diag
 131083; Y08763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
 131148; AW953575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
 131216; AI815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag
 131226; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
 131244; AI638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
 131289; AA298896; Hs.333418; FXVD domain-containing lon tra; colon; diag
 131307; NM_000025; Hs.2548; adrenergic, beta-3-, receptor; EWS; mAb
 131313; R96290; Hs.76874; ribosomal protein L44; EWS; diag
 131492; AJ452801; Hs.288869; nuclear receptor subfamily 2, ; pros; mAb+s.m.
 131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag
 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
 131643; AW410801; Hs.30026; HSPC182 protein; breast; diag
 131739; AF077986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

- 131817; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, gill; s.m.
 131885; BE602341; Hs.3402; ESTs; breast; diag
 131919; T15803; Hs.272458; protein phosphatase 3 (former); pros; breast; s.m.
 131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag
 131965; W79283; Hs.35982; ESTs; lung, ovar; diag
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 132050; AJ267615; Hs.38022; ESTs; angio; diag
 132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag
 132180; NM_004460; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 f; ovar; diag
 132349; AW975654; Hs.181286; serine protease inhibitor; Kaz; pros; blad; s.m.
 132354; BE185289; Hs.1076; small proline-rich protein 1B; lung; diag
 132358; NM_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.
 132371; AA235448; Hs.222088; PRO2000 protein; breast; diag
 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
 132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
 132520; AA257992; Hs.50851; Janus kinase 1 (a protein tyro; EWS; s.m.
 132528; T76736; Hs.50758; SMC4 (structural maintenance c; ovar; CTL+s.m.
 132543; BE588452; Hs.344037; protein regulator of cytokines; colon, lung; diag
 132572; A1929659; Hs.237825; signal recognition particle 72; ovar; diag
 132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 f; colon; diag
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
 132632; AJ076916; Hs.5398; guanine monophosphate synthetase; ovar, lung; s.m.
 132669; W38688; Hs.380933; guanine nucleotide binding pro; colon; diag
 132710; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, colon, headnk; diag
 132725; NM_006276; Hs.184167; splicing factor, arginine/ser; ovar; CTL+s.m.
 132767; BE182592; Hs.11261; small proline-rich protein 2A; lung; diag
 132791; AB029561; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
 132837; AA370362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag
 132858; NM_001448; Hs.58367; glypican 4; breast, colon, pros; mAb
 132888; NM_005478; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
 132902; AJ96442; Hs.5938; hypothetical protein FLJ10808; colon; diag
 132939; AB009284; Hs.61152; exostosin (multiple)-like 2; ovar; diag
 132984; A1362575; Hs.303171; ESTs; pros; diag
 132987; AA316181; Hs.61635; six transmembrane epithelial c; pros, pros; mAb+CTL
 132990; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung; CTL+s.m.
 132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
 133006; AW878436; Hs.62515; KIAA0494 gene product; colon; diag
 133016; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactose; breast, colon, pros; s.m.
 133018; A143688; Hs.6289; hypothetical protein FLJ20886; breast; diag
 133051; A186431; Hs.256638; prostate differentiation facto; angio, pros, blad; diag
 133063; A1654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
 133070; U92849; Hs.380136; a disintegrin and metalloprote; leuc; diag
 133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
 133260; AA403046; Hs.6906; Homo sapiens cDNA: FLJ23197 f; angio; diag
 133272; NM_002776; Hs.69423; kalikrein 10; colon, ovar; diag
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
 133321; T79526; Hs.179516; integral type 1 protein; breast; diag
 133391; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag
 133415; X69699; Hs.73149; paired box gene 6; ovar; CTL
 133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
 133579; X75348; Hs.75074; mitogen-activated protein kinase; pros; diag
 133626; AW836130; Hs.75277; hypothetical protein FLJ13810; pros; diag
 133738; D49958; Hs.75819; glycoprotein MGA; pros; mAb
 133829; AW630080; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; ovar; diag
 133860; S78256; Hs.76888; hypothetical protein MGC12702; blad; diag
 133944; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag
 133978; AJ908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
 134100; AA460085; Hs.171075; replication factor C (activator; pros; diag
 134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
 134169; A1690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.
 134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
 134319; BE304999; Hs.285764; fumarate hydratase; colon; s.m.
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
 134348; AW291946; Hs.82066; Interleukin 6 signal transduce; breast; mAb+s.m.
 134374; N22687; Hs.8238; ESTs; pros; diag
 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
 134401; A1916662; Hs.211577; kinesin 1 (kinesin receptor); pros, breast; mAb+s.m.
 134405; AW076003; Hs.82772; collagen, type XI, alpha 1; breast, lung, ovar, headnk; CTL
 134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.
 134528; AW411479; Hs.848; FK506-binding protein 4 (59kD); breast; diag
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
 134654; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
 134691; AW382987; Hs.88474; prostaglandin-endoperoxide syn; ovar; s.m.
 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
 134731; D89377; Hs.89404; msh (Drosophila) homeo box form; blad; s.m.
 134756; T28618; Hs.89640; TEK tyrosine kinase, endothel; angio; s.m.
 134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin; blad; mAb
 134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.

- 134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 134924; BE294029; Hs.279903; Ras homolog enriched in brain; breast; mAb
 134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.
 134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag
 134889; AW968058; Hs.92381; nudix (nucleoside diphosphate); colon; diag
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10661 fis; breast; diag
 135166; AA136867; Hs.280858; ESTs, Highly similar to A35661; pros; diag
 135235; AW298244; Hs.286195; ESTs; angio; diag
 135242; A1583187; Hs.9700; cyclin E1; ovar; CTL+s.m.
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
 135255; Y13645; Hs.97234; uroplakin 2; blad; mAb
 135309; A1564123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag
 135315; H81138; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag
 135389; U05237; Hs.99872; fetal Alzheimer antigen; pros; breast, colon; CTL+s.m.
 135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros; breast; mAb+s.m.
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1_H; angio; CTL+diag
 300605; A1218847; Hs.152670; ESTs; pros; diag
 300921; AF146747; Hs.232185; polycythemia rubra vera 1; cel; pros; mAb+s.m.
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
 301042; A1859131; Hs.365053; hypothetical protein MGC2849; pros; mAb
 301043; A1180316; Hs.149155; voltage-dependent anion channel; pros; mAb+s.m.
 301050; AW136973; Hs.362915; ESTs, Weakly similar to S68890; colon, lung; CTL+s.m.
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast, lung; mAb+s.m.
 302001; AB020711; Hs.374965; KIAA0904 protein; breast; CTL+s.m.
 302005; BE252922; Hs.123119; MAD (mothers against decapenta; pros; diag
 302057; BE542706; Hs.222399; CEGP1 protein; breast; diag
 302167; NM_006227; Hs.283007; phospholipid transfer protein; pros; mAb
 302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb+s.m.
 302280; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros; breast; diag
 302372; AL117406; Hs.335891; ATP-binding cassette transport; breast; pros; mAb+s.m.
 302384; A1678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 302410; NM_004917; Hs.218366; kallikrein 4 (protease, enamel; pros; diag
 302468; AL133561; Hs.380156; DKFZP434B081 protein; pros; diag
 302582; BE149762; Hs.48956; gap junction protein, beta 6 (); lung, blad; mAb
 302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 303295; AA205625; Hs.206067; ESTs; blad; diag
 303380; AW962764; Hs.303171; olfactory receptor, family 51.; pros; mAb
 303505; AA340805; Hs.105887; ESTs, Weakly similar to Homolo; pros; breast, colon; diag
 303699; BE143707; Hs.19525; hypothetical protein FLJ2794; pros; diag
 303753; AW503733; Hs.9414; KIAA1488 protein; pros; breast, colon; CTL+s.m.
 305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag
 306273; AA836290; ; gbion70a01.st Soares_NFL_T_GBC; pros; diag
 306676; A1005603; ; gbion15c10.s1 NCI_CGAP_GC3 Hom; lung; diag
 306840; AN077477; Hs.307912; ESTs; angio; diag
 309177; A0951118; Hs.326736; Homo sapiens breast cancer ant; breast, pros; mAb+CTL
 309583; AW170036; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 309931; AW341683; Hs.343663; gbhd13d01.x1 Soares_NFL_T_GBC; lung; mAb
 310382; A1734009; Hs.127699; KIAA1603 protein; pros; diag
 310431; A1420227; Hs.368053; ESTs, Weakly similar to A46010; pros; diag
 310573; AW292180; Hs.156142; ESTs; pros; diag
 310636; A1814373; Hs.164176; ESTs; lung; diag
 310781; A1380797; Hs.168892; ESTs; breast; diag
 310955; A1476732; Hs.263912; ESTs; breast, angio; diag
 311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD_H; lung; mAb+s.m.
 311166; A1821005; Hs.118599; Intron of: BFF9 (GDNFRa); breast; diag
 311251; A1655662; Hs.197698; ESTs; pros; diag
 311557; AF200492; Hs.211238; interleukin-1 homolog 1; lung; diag
 311596; A1682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 311630; A1915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 311877; AA084248; Hs.372651; G protein-coupled receptor 39; ovar, angio, glio; mAb+s.m.
 311911; R19176; Hs.169793; ribosomal protein L32; pros; diag
 311828; T62216; Hs.378028; ESTs; pros; diag
 312182; T94344; Hs.326263; ESTs; pros; diag
 312252; A128386; Hs.143866; ESTs; blad; diag
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
 312521; A1263307; Hs.356901; H2B histone family, member L; pros; breast, lung; diag
 312544; AA516420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag
 312742; A1650363; Hs.116462; ESTs; colon; diag
 312795; AW975014; Hs.28; ferrochelatase (protoporphyrin; pros; s.m.
 312857; BE083868; Hs.126914; KIAA1430 protein; colon, pros; CTL+s.m.
 312922; AA329258; Hs.378739; ESTs, Moderately similar to al; pros; diag
 313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 313556; AA628517; Hs.118502; ESTs; angio; diag
 313665; AW751201; Hs.120932; ESTs; angio; diag
 313774; A1916058; Hs.144583; ESTs; colon; CTL
 313915; C18883; Hs.163443; intron of perlestin (OSF-2os); breast; diag
 313978; A1870175; Hs.13957; ESTs; angio; diag
 314078; AW129357; Hs.329700; ESTs; breast; diag

- 314097; AA648744; Hs.269493; ESTs; breast; diag
 314121; AI732083; Hs.187619; ESTs; pros; breast; diag
 314171; AI821895; Hs.193481; ESTs; pros; diag
 314508; AA833656; Hs.206868; Homo sapiens cDNA FLJ14056 f1; breast; diag
 314547; AA399272; Hs.144341; ESTs; breast; diag
 314558; AI873274; Hs.370280; ESTs; breast; pros; diag
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 f1; lung, blad; diag
 314691; AW207208; Hs.356962; ESTs; breast; pros; diag
 314785; AI538226; Hs.32976; guanine nucleotide binding pro; colon; pros; diag
 314907; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 315008; AI536613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 315033; AI493048; Hs.146133; ESTs; colon; diag
 315051; AW292425; Hs.163484; ESTs; breast, pros; blad; diag
 315052; AA876910; Hs.134427; ESTs; pros; breast; diag
 315198; AI367347; Hs.44889; Homo sapiens clone TCCCTA00151; breast; diag
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
 315408; AW273261; Hs.216292; ESTs; pros; diag
 315634; AA837085; Hs.372254; ESTs; breast, pros; diag
 315720; AA292998; Hs.163900; ESTs; blad; diag
 316177; AG04982; Hs.293102; downstream of breast cancer an; breast; mAb+CTL
 316442; AA760894; Hs.125350; ESTs; pros; diag
 316580; AA936198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.
 316886; AA836331; Hs.170261; ESTs; breast; diag
 316943; AW014875; Hs.137007; ESTs; blad; diag
 317078; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
 317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 f1; breast; diag
 317224; X73608; Hs.93029; sparcksteonectin, oocyte and ka; pros; angio; diag
 317548; BE66568; Hs.159066; ESTs; pros; CTL+s.m.
 317803; AW684964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.
 317881; AI827248; Hs.224398; Homo sapiens cDNA FLJ11469 f1; breast, lung; diag
 318240; AI085377; Hs.143610; ESTs; lung; diag
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros; colon; CTL+s.m.
 318532; AW139377; Hs.127179; cryptic gene; panc; diag
 318744; AI793124; Hs.144479; ESTs; breast; diag
 318754; W21423; Hs.44222; CGI-80 protein; pros; diag
 319080; AW987648; Hs.23023; ESTs; pros; diag
 319795; AB037821; Hs.146858; protocadherin 10; pros, glio; mAb+s.m.
 320066; BE305242; Hs.16098; claudin 2; colon, panc; diag
 320167; AA984373; Hs.80790; Homo sapiens cDNA: FLJ22930 f1; breast, pros; diag
 320203; AL049227; Hs.124778; downstream of cadherin 6 (by 3; renal, ovar; mAb+s.m.
 320211; AL039402; Hs.125783; DME-6 protein; breast, pros; CTL
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb
 320561; AF085808; Hs.159330; uropodkin 3; pros; blad; diag
 320590; U67068; Hs.154298; Human proteinase activated rec; pros; mAb+s.m.
 320635; N50617; Hs.80508; small nuclear ribonucleoprotein; angio lung; diag
 320738; AA315381; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 320786; AK001641; Hs.31218; secretory carrier membrane pro; pros; colon; diag
 320896; BE019924; Hs.271580; uropodkin 1B; lung, blad, ovar, headnk; mAb+diag
 321023; AW294318; Hs.125608; ESTs; colon; diag
 321107; AI732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
 321412; AI674383; Hs.22891; solute carrier family 7 (catio; pros; mAb+s.m.
 321441; AF107493; Hs.201676; Homo sapiens LUCA-15 protein m; pros; breast; diag
 321644; AW975944; Hs.237396; ESTs; breast, pros; diag
 321717; AW956580; Hs.42689; ESTs; angio; diag
 321908; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
 322035; AL137517; Hs.306201; hypothetical protein DKFZp584C; breast, blad; mAb
 322521; AF147347; ; gb:Homo sapiens full length In; breast; diag
 322706; AA018889; Hs.127179; cryptic gene; panc; diag
 322782; AA058060; Hs.202577; Homo sapiens cDNA FLJ12166 f1; pros; diag
 322818; AW043782; Hs.293616; ESTs; pros, breast, angio, glio; diag
 322882; AW248508; Hs.278727; Homo sapiens cDNA FLJ14035 f1; breast, lung, ovar, angio, blad; diag
 322975; C16391; ; Intron of breast cancer antigen; breast; mAb+CTL
 323188; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast; diag
 323226; AF055019; Hs.355279; Homo sapiens clone 24670 mRNA; pros; diag
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 323332; AI829520; ; gb:W19c06.x1 NCL CGAP_U11 Hom; breast; diag
 323335; AI655499; Hs.181712; ESTs; pros; breast; mAb
 323587; AI299709; Hs.131886; Homo sapiens cDNA: FLJ22113 f1; colon; diag
 323817; AA410843; ; NAME OMITTED ... receptor kinase; breast; mAb
 324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag
 324295; AA434578; Hs.143891; ESTs; pros; diag
 324338; AA827668; Hs.145078; regulator of differentiation (; colon; diag
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 f1; pros; colon; diag
 324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag
 324603; AW993522; Hs.299887; ESTs; pros; breast; diag
 324817; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros; diag
 324858; AI694787; Hs.129179; Homo sapiens cDNA FLJ13581 f1; pros; diag
 324718; AI557019; Hs.116467; small nuclear protein PRAC; colon; pros; diag
 324866; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
 324871; AI890347; Hs.271923; Homo sapiens cDNA: FLJ22785 f1; colon; diag

- 324987; AI375572; Hs.172634; ESTs; breast; diag
 325372; ; Phase 2 & 3 Exons; breast; CTL+s.m.
 325544; ; Phase 2 & 3 Exons; breast; angio; diag
 327038; ; Phase 2 & 3 Exons; lung; angio; diag
 327075; ; Phase 2 & 3 Exons; breast; lung; diag
 327414; ; Phase 2 & 3 Exons; angio; diag
 328700; ; Phase 2 & 3 Exons; breast; angio; diag
 330211; ; Phase 2 & 3 Exons; pros; CTL+s.m.
 330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung, colon, blad; diag
 330493; M27828; Hs.334372; endogenous retroviral protease; lung, colon; s.m.
 330630; NM_002802; Hs.79088; redocalbin 2; EF-hand calc; pros; diag
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
 330790; AI660243; Hs.318545; Hu01 Chip Redos; pros; blad; diag
 330814; AI955040; Hs.265396; PAR-6 beta (partitioning def; breast; diag
 330827; AI961486; Hs.249196; ESTs; lung, uter; diag
 330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag
 331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag
 331151; R82331; Hs.121602; ESTs; pros; breast; diag
 331183; T40769; Hs.8469; ESTs; colon; diag
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 f1; angio; diag
 331490; AF218751; Hs.26813; CDA14; pros; diag
 331578; AI246482; Hs.243010; ESTs; angio; diag
 331614; N92293; Hs.208832; EST; Moderately similar to ALU; breast; diag
 331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag
 331889; AA677677; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast; lung; CTL
 332180; AF134160; Hs.7327; claudin 1; lung; mAb
 332247; AA665097; ; ESTs; pros; breast; diag
 332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag
 332453; L12583; Hs.334309; Hu01 Chip Redos; lung; diag
 332468; AB018258; Hs.118140; KIAA0718 gene product; angio; diag
 332530; M31669; Hs.1735; Inhibin; beta B (activin AB be; ovar; pros; diag
 332535; AF167708; Hs.19280; cysteine-rich repeat-containing; angio; diag
 332640; BE668452; Hs.344637; protein regulator of cytokines; blad, headnk; diag
 332645; AA284371; Hs.118064; ESTs; breast; colon; diag
 332686; X69699; Hs.73149; paired box gene B; ovar; CTL+s.m.
 332697; X51405; Hs.76360; carboxypeptidase E; pros; diag
 332740; BE409669; Hs.266241; Homo sapiens cDNA: FLJ22698 f1; pros; diag
 332798; ; C22000007.g11231419[emb]CAB9; pros; breast; diag
 333769; ; NM_005940*Homo sapiens matrix; breast, colon, lung; mAb+diag+s.m.
 335904; ; Chromosome 22; pros; diag
 334223; ; NM_005080*Homo sapiens X-box; pros; breast; diag
 334447; ; NM_012429*Homo sapiens SEC14; pros; diag
 335115; ; NM_006498*Homo sapiens lectin; pros; CTL+s.m.
 335809; ; NM_014509*Homo sapiens kraken; breast; CTL+s.m.
 335824; ; ENSP00000248072*DJ222E13.1 (N); breast; pros; CTL+s.m.
 335825; ; ENSP00000249072*DJ222E13.1 (N); breast; diag
 335938; ; Chromosome 22; lung; diag
 336034; ; NM_007172*Homo sapiens nucleop; breast; angio; CTL+s.m.
 336152; ; NM_014246*Homo sapiens cadherin; breast; mAb
 336836; ; C22000024.g11064530[gb]AAG2; lung, breast; CTL+s.m.
 338008; ; NM_005940*Homo sapiens matrix; lung, breast, colon; mAb+diag+s.m.
 338033; ; Chromosome 22; lung; angio; diag
 338158; ; NM_012399*Homo sapiens phosph; lung, angio; diag
 338255; ; NM_014323*Homo sapiens zinc f; pros, breast, colon; CTL+s.m.
 400195; ; Hs.42850; NM_007057*Homo sapiens ZW10 f; lung; CTL+s.m.
 400269; ; Hs.253495; Eos Control; fibro; diag
 400285; ; Eos Control; lung; diag
 400287; S39329; Hs.181350; kallikrein 2, prostetic; pros; diag
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb
 400294; N95796; Hs.278695; Homo sapiens protein mRNA, cc; pros, pros; mAb
 400295; W72838; Hs.348419; AI905687; L-BT095-190199-019 B; breast; diag
 400298; AA032279; Hs.61635; six transmembrane epithelial s; panc, lung, headnk, stom, EWS, ovar; mAb+CTL
 400328; X87344; ; transporter 2, ATP-binding cas; lung; mAb+s.m.
 400409; AF153341; ; Homo sapiens winged helixfork; blad; CTL+s.m.
 400419; AF084545; ; Target; lung, sarc; diag
 400440; X83957; Hs.83870; nebulin; sarc; diag
 400494; ; ENSP00000238970*CI630 (Fragme; angio; mAb
 400517; ; lengain; stom, cerv, uter, lung, pros, colon, hepC; diag
 400651; ; ENSP00000228031*COOPER CHAPER; sarc; s.m.
 400685; ; NM_002425*Homo sapiens matrix; lung; mAb+diag+s.m.
 400773; ; NM_003105*Homo sapiens sorit; blad; mAb
 400844; ; NM_003105*Homo sapiens sorit; blad; s.m.
 400846; ; soritin-related receptor, L1D; blad; mAb+s.m.
 400881; ; NM_025080*Homo sapiens hypoth; ovar; diag
 401093; ; C12000586.g16330167[db]9AA8; blad, lung; CTL+s.m.
 401234; ; mitogen-activated protein kinase; angio; diag
 401424; ; NM_001172*Homo sapiens arginase; pros; s.m.
 401488; ; C4000647.g14758508[ref]NP_00; headnk; mAb
 401704; ; NM_021185*Homo sapiens claudin; test; mAb
 401732; ; NM_001176*Homo sapiens Rho GD; panc; diag
 401747; ; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, melar; diag

- 401760; ;; Target Exon; blad, lung, headnk, esoph; diag
 401760; ;; NM_005557*:Homo sapiens kerat1; lung, blad, headnk, esoph, mela; diag
 401781; ;; Target Exon; lung, blad, headnk, esoph, cerv; diag
 401785; ;; NM_002275*:Homo sapiens kerat1; lung; diag
 5 401797; ;; Target Exon; sarc; diag
 401894; ;; Target Exon; lung; diag
 402145; ;; Target Exon; test; CTL+s.m.
 402199; ;; Target Exon; test; CTL+s.m.
 10 402230; ;; Fgenesh predicted: CYTOCHROME ; blad; diag
 402239; ;; Target Exon; blad; diag
 402260; ;; NM_001436*:Homo sapiens fibr1; blad; CTL+s.m.
 402265; ;; Target Exon; lung; diag
 402305; ;; C19000735*.g|4508027|refNP_0; blad; CTL+s.m.
 15 402420; ;; C1000823*.g|1043240|emb|CAC1; lung; diag
 402424; ;; NM_024901*:Homo sapiens hypothe; blad; CTL+s.m.
 402447; ;; C1000201.g|204416|gb|AAA02627; esoph; mAb
 402474; ;; NM_004078*:Homo sapiens catheps; lung, colon, stom, fibro; diag
 402550; ;; Target Exon; fibro; diag
 20 402604; ;; Target Exon; glio; diag
 402605; ;; Target Exon; glio; diag
 402606; ;; NM_024626*:Homo sapiens hypothe; ovar, breast; mAb
 402680; ;; Target Exon; test; mAb
 402777; ;; C1002652*.g|544327|sp|C04799; blad; diag
 25 402860; ;; ENSP00000239210:DJ50024.4 (nov; mela; CTL+s.m.
 402888; ;; Target Exon; sarc; diag
 402992; ;; Target Exon; sarc; diag
 402994; ;; NM_002463*:Homo sapiens myxov; esoph; diag
 403046; ;; NM_005656*:Homo sapiens transn; pros; mAb
 403047; ;; NM_005656*:Homo sapiens transn; pros, blad, colon; mAb
 30 403071; ;; NM_003319*:Homo sapiens tlin; sarc; diag
 403088; ;; NM_003319*:Homo sapiens tlin; sarc; diag
 403171; ;; C2001472*.g|5609678|gb|AAB418; test; diag
 403326; ;; Target Exon; mela; diag
 35 403329; ;; unnamed protein product [Homo ; lung; diag
 403381; ;; ENSP00000231844*:Ecotropic vir; blad; CTL+s.m.
 403409; ;; NM_005929*:Homo sapiens antigen; mela; mAb
 403433; ;; NM_001622*:Homo sapiens alpha-2; hepC; diag
 403476; ;; NM_022342*:Homo sapiens kinase; lung; CTL+s.m.
 40 403715; ;; Target Exon; lung; diag
 403740; ;; NM_001076*:Homo sapiens UDP gl; pros, hepC; s.m.
 403776; ;; ENSP00000226542*:Small Inductib; panc; diag
 403903; ;; C5001632*.g|10645308|gb|AAG21; blad; CTL+s.m.
 404029; ;; NM_018936*:Homo sapiens protoc; glio; mAb
 404049; ;; NM_018937*:Homo sapiens protoc; glio; mAb
 45 404210; ;; NM_005938*:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
 404240; ;; NM_018950*:Homo sapiens major h; fibro; mAb
 404263; ;; NM_021058*:Homo sapiens H2B h; lung; CTL+s.m.
 404288; ;; C8001909.g|704441|db|BAA1890; panc; diag
 404298; ;; C6001238*.g|121715|sp|P26697; lung; s.m.
 50 404403; ;; Target Exon; blad; diag
 404440; ;; NM_021048*:Homo sapiens melanom; lung, blad; mAb+CTL
 404866; ;; ENSP00000251112*:Sodium/potass; panc; s.m.
 404877; ;; NM_005365*:Homo sapiens melanom; lung, blad; CTL+s.m.
 55 404927; ;; Target Exon; lung, headnk; diag
 404996; ;; Target Exon; lung, headnk, esoph; diag
 405001; ;; interleukin enhancer binding f; sarc; diag
 405025; ;; Homo sapiens bone morphogenetic; angio; diag
 405121; ;; mitogen-activated protein kina; angio, renal; s.m.
 60 405238; ;; Target Exon; glio; diag
 405239; ;; oxidative 3 alpha hydroxyster; glio; s.m.
 405451; ;; Homo sapiens glutamyl-peptid; mela; s.m.
 405455; ;; Target Exon; cerv; mAb
 405546; ;; NM_018833*:Homo sapiens transp; cerv; mAb
 65 405547; ;; NM_018833*:Homo sapiens transp; cerv, mela; mAb
 405646; ;; C12000200.g|4557225|refNP_00; lung; diag
 405704; ;; NM_001844*:Homo sapiens collag; sarc; diag
 405770; ;; NM_002352*:Homo sapiens melanom; lung, esoph; mAb+CTL
 405849; ;; Target Exon; panc; diag
 70 405932; ;; C15000305.g|3806122|gb|AAC691; blad, lung, headnk, cerv; CTL+s.m.
 406081; ;; Target Exon; blad; diag
 406137; ;; NM_000179*:Homo sapiens mutS f; lung; CTL+s.m.
 406173; ;; ENSP00000250148*:Growth hormon; panc; CTL+s.m.
 406348; ;; Target Exon; breast; CTL+s.m.
 75 406360; ;; Target Exon; lung, headnk; diag
 406399; ;; NM_003122*:Homo sapiens serine; blad; diag
 406434; ;; NM_030579*:Homo sapiens cytoch; blad; diag
 406467; ;; Target Exon; lung, headnk, blad; diag
 406506; ;; Target Exon; angio; diag
 80 406547; ;; Target Exon; test; diag
 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte; panc; mAb
 406672; M26041; Hs.198253; major histocompatibility comp; fibro; mAb
 406685; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

- 406587; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
 406590; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
 406906; Z25424; ; gb:Human protein-serine/th; blad, lung; s.m.
 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
 406987; M24348; ; gb:Human parathyroid hormone-1; lung; CTL+s.m.
 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial; sarc; diag
 407034; U84540; ; gb:Human dystrobrevin isoform 1; gl; diag
 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
 407118; AA156790; Hs.262036; ESTs, Weakly similar to Z223_H; pros; diag
 407122; H20276; Hs.31742; ESTs; pros; diag
 407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag
 407166; R45175; Hs.117183; ESTs; pros, breast, colon; diag
 407176; AA195651; Hs.352312; AP-2 beta transcription factor; breast; CTL+s.m.
 407202; N58172; Hs.109370; ESTs; pros; diag
 407216; N91773; Hs.348385; lysyl oxidase; panc; diag
 407242; M18720; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb
 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
 407245; X90568; Hs.172004; filin; sarc; diag
 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
 407262; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
 407276; A1951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 407289; AA135159; Hs.203348; Homo sapiens cDNA FLJ12149 f5; lung; diag
 407368; AF026942; Hs.17518; gb:Homo sapiens c1g33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag
 407581; R49402; Hs.173508; P3ECSL; blad; CTL+s.m.
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
 407710; AW022727; Hs.23616; ESTs; test; diag
 407720; AB037776; Hs.38302; KIAA1355 protein; lung; mAb
 407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag
 407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.
 407768; D50815; Hs.38365; KIAA0125 gene product; lung; diag
 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
 407782; AA608958; Hs.112819; ESTs, Moderately similar to PU; lung; diag
 407786; AA667538; Hs.38872; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb
 407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.
 407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 f5; sarc; diag
 407839; AA045144; Hs.161696; ESTs; blad, headnk; mAb
 407846; AA426202; Hs.40403; Cbp/p300-interacting transact; mela; diag
 407853; AA336797; Hs.40498; diolclop (Xenopus laevis) homo; colon, stom, renal, breast, ovar, uter, cerv; diag
 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
 407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb
 407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.
 407910; AA650274; Hs.41296; fibronectin leucine rich trans; fibro; mAb
 407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb
 407948; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro; blad; diag
 407962; A1135530; Hs.62930; ESTs, Weakly similar to S69501; angio; mAb+s.m.
 408000; L11690; Hs.198699; bullous pemphigoid antigen 1 (s; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
 408045; AW136859; Hs.245123; ESTs; breast; diag
 408056; AA312329; Hs.42331; ephrin-A4; ovar; diag
 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
 408081; AW451697; Hs.167409; Intron of basic-helix-loop-hel; ovar, gl; diag
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.
 408122; A1432652; Hs.42624; hypothetical protein FLJ10718; lung; diag
 408209; NM_004454; Hs.43697; ets variant gene 5 (ets-relate; mela; CTL+s.m.
 408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
 408308; AL033377; Hs.44197; hypothetical protein DKFZP5640; panc, renal, colon; mAb
 408353; BE439638; Hs.44298; mitochondrial ribosomal protel; lung; diag
 408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26, ; pros; mAb
 408522; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, esoph, cerv; diag
 408561; A1308037; Hs.84120; hypothetical protein MGC13016; mela; CTL+s.m.
 408570; AL046408; Hs.103483; KIAA1798 protein; angio; CTL+s.m.
 408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag
 408591; AF016224; Hs.46452; mammaglobin 1; breast, cerv; diag
 408611; NM_004367; Hs.46458; chemokine (C-C motif) receptor; mela; mAb
 408633; AW963372; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag
 408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
 408728; AL137378; Hs.47125; hypothetical protein FLJ13912; test; diag
 408758; NM_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.
 408770; AW270608; Hs.170195; bone morphogenetic protein 7 (s; ovar; mAb+diag
 408771; AW732573; Hs.47584; potassium voltage-gated channel; lung; mAb
 408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag
 408795; AW749128; Hs.170345; hypothetical protein FLJ13710; ovar; diag
 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
 408833; AW612232; Hs.254835; ESTs; pros; diag
 408877; AA479033; Hs.130315; ESTs, Weakly similar to A47682; breast; diag
 408915; NM_018651; Hs.48950; hepatocellular carcinoma novel ; panc, sarc; diag
 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

- 408962; BE388436; Hs.44317; SRY (sex determining region Y); meta; diag
 408992; AA059325; Hs.30114; guanine nucleotide binding protein; lung; diag
 408996; A979168; Hs.82226; glycoprotein (transmembrane); meta; mAb+s.m.
 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarco; CTL+s.m.
 409038; T97490; Hs.50002; small inducible cytokine subfamily; meta; diag
 409051; AA060912; gbzn04d03.r1 Stratagene hNT n; pros; s.m.
 409077; AA063037; Hs.66803; ESTs; lung; diag
 409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
 409123; AA063403; gbzm04d12.s1 Stratagene corn; pros; s.m.
 409142; AL136877; Hs.50756; SMC4 (structural maintenance of; ovar, lung, meta; diag
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
 409200; AL042914; Hs.51039; KIAA0076 gene product; sarco; CTL+s.m.
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag
 409228; R16811; Hs.22010; ESTs, Weakly similar to 210928; lung; mAb
 409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros, ovar, breast, uter, panc, colon, stom; mAb
 409243; AB037781; Hs.51743; KIAA1340 protein; test; diag
 409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
 409264; NM_014937; Hs.52463; KIAA0966 protein; meta; CTL+s.m.
 409268; AA578953; Hs.22972; steroid 5 alpha-reductase 2-ii; breast, ovar, lung, panc, uter; mAb
 409327; L41162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarco; CTL+s.m.
 409340; BE174529; Hs.321130; hypothetical protein MGC2771; meta; CTL+s.m.
 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
 409348; AJ401533; Hs.146090; ESTs; renal, glio; diag
 409361; NM_005982; Hs.54416; sine oculis homeobox (Drosophila); blad, lung, pros; CTL+s.m.
 409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome; glio; diag
 409395; U46745; Hs.338678; dystrobrevin, alpha; glio; diag
 409402; AF208234; Hs.695; cystatin B (steffin B); blad; diag
 409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 f1; meta; diag
 409421; AA199883; Hs.87824; ESTs; test; diag
 409430; R21945; Hs.346735; splicing factor, arginine/serine; meta; diag
 409432; D49372; Hs.54460; small inducible cytokine subfamily; stom, esoph; diag
 409433; AA074382; Hs.135255; ESTs; glio, sarco; diag
 409509; AL036923; Hs.322710; ESTs; angio; diag
 409512; AW979187; Hs.293591; melanoma differentiation assoc; meta, esoph; CTL+s.m.
 409542; AA503020; Hs.35563; hypothetical protein FLJ22418; breast, ovar; diag
 409562; R27430; Hs.271555; ESTs; lung; diag
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, meta, sarco; CTL+s.m.
 409633; AW449822; Hs.55200; ESTs; sarco; diag
 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag
 409638; AW450420; Hs.21335; ESTs; glio; diag
 409670; AJ368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.
 409703; NM_006187; Hs.56009; 2'-5'-oligoadenylate synthetase; panc, esoph, meta; s.m.
 409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
 409719; AJ769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag
 409731; AA125985; Hs.56145; thymosin, beta, identified in; pros, sarco; CTL+s.m.
 409745; AA077391; gb:7B14E12 Chromosome 7 Fetal; ovar, renal; CTL+s.m.
 409935; AW511413; Hs.187393; ESTs; lung; diag
 409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
 409988; N27687; Hs.334334; transcription factor AP-2 alpha; meta; diag
 410006; AW732368; Hs.57783; eukaryotic translation Initiat; test; diag
 410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
 410044; BE566742; Hs.58185; highly expressed in cancer, rt; blad; diag
 410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.
 410076; T05387; Hs.7991; ESTs; lung, pros; diag
 410079; U94562; Hs.380757; glycogenin 2; meta; diag
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag
 410102; AW248508; Hs.279727; ESTs; homologues of PEM-3 (Cion; ovar, breast, blad, lung, angio, sarco; diag
 410174; AA306007; Hs.58461; DKFZP434C245 protein; meta; diag
 410240; AL157424; Hs.61289; synaptotagmin 2; angio; diag
 410247; AF181721; Hs.61345; RU25; ovar; CTL+s.m.
 410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; meta; diag
 410310; J02931; Hs.62192; coagulation factor III (thromb; pros, panc; mAb
 410381; BE391804; Hs.62661; guanylate binding protein 1, l; meta, esoph, hepC, fibro, uter; diag
 410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
 410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb
 410491; AA485131; Hs.64001; Homo sapiens clone 25218 mRNA; meta, esoph; diag
 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb
 410553; AW016824; Hs.272088; hypothetical protein MGC14128; blad, lung; diag
 410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb
 410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 f1; lung; diag
 410588; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 f5; panc; diag
 410600; AW575742; Hs.351676; ESTs, Moderately similar to S8; meta; mAb+s.m.
 410621; AA194328; Hs.172004; ttfu; sarco; diag
 410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag
 410687; U24388; Hs.65436; lysyl oxidase-like 1; panc; diag
 410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL
 410763; AF279145; Hs.8968; hypothetical protein FLJ21778; panc; mAb
 410865; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
 410867; X63598; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
 410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

- 410889; X91662; Hs.66744; twist (Drosophila) homolog (ac; sarc; CTL+s.m.
 410929; H47233; Hs.30643; ESTs; ovar; test; diag
 411076; A1222020; Hs.182364; CocoaCrisp; pros; glio; breast; diag
 411089; AA456454; Hs.214291; cell division cycle 2-like 1 l; lung; fibro; CTL+s.m.
 411243; AB039886; Hs.69319; CA11; esoph; diag
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fis; blad; diag
 411257; AA628967; Hs.115274; Indian hedgehog protein (IHH); ovar; diag
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centric; lung; blad; headnk; CTL+s.m.
 411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag
 411358; R47479; Hs.94761; KIAA1691 protein; mela; renal; sarc; mAb
 411388; X72925; Hs.69752; desmocollin 1; headnk; mela; mAb
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMENT); ovar; diag
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc; pros; stom; breast; uter; cerv; ovar; mAb
 411573; AB029000; Hs.70823; KIAA1077 protein; panc; headnk; lung; stom; diag
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
 411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag
 411768; NM_013371; Hs.71979; Interleukin 19; ovar; uter; cerv; diag
 411789; AF245505; Hs.72157; Adipican; breast; panc; lung; stom; headnk; ovar; uter; esoph; sarc; diag
 411825; AK000334; Hs.352416; solute carrier family 39 (zinc; colon; ovar; mAb
 411828; AW181449; Hs.72290; wingless-type MMTV Integration; ovar; diag
 411869; W20027; Hs.23439; ESTs; angio; diag
 411874; AA096106; Hs.20403; ESTs; blad; diag
 411880; AW872477; ; gclm3003.x1 NCL CGAP_Thy4 Ho; blad; diag
 411945; AL033527; Hs.92137; L-myo-2 protein (MYCL2); blad; ovar; CTL+s.m.
 412006; AW451618; Hs.380583; ESTs; sarc; diag
 412026; AA383618; Hs.73073; testis-specific ankyrin motif; test; diag
 412045; AA099802; Hs.83883; transmembrane, prostate endog; pros; mAb+s.m.
 412099; U64198; Hs.73165; Interleukin 12 receptor, beta; leuk; mela; mAb
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc; fibro; diag
 412116; AK001763; Hs.73239; hypothetical protein FLJ10901; lung; blad; CTL+s.m.
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
 412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb
 412225; AW503785; Hs.73792; complement component (3d/Epste; mela; mAb
 412247; AF022375; Hs.73793; vascular endothelial growth fa; renal; glio; blad; colon; diag
 412265; AA101325; Hs.88154; hypothetical protein FLJ12457; test; CTL+s.m.
 412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros; leuk; diag
 412351; AL135950; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.
 412420; AL035868; Hs.73853; bone morphogenetic protein 2; blad; glio; lung; stom; angio; diag
 412448; L12964; Hs.73896; tumor necrosis factor receptor; leuk; mAb
 412471; M63193; Hs.73946; endothelial cell growth factor; cerv; mela; esoph; diag
 412490; AW803554; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; mela; diag
 412518; AA196241; Hs.73980; Irfonin T1, skeletal, slow; sarc; diag
 412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad; lung; diag
 412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
 412580; AA113262; Hs.17901; similar to CABLES [Homo saplen; mela; diag
 412610; X90908; Hs.74126; fatty acid binding protein 6; ; blad; diag
 412661; N32860; Hs.24611; ESTs, Weekly similar to I54374; blad; CTL+s.m.
 412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
 412723; AA648488; Hs.335951; hypothetical protein AF301222; lung; blad; headnk; colon; stom; uter; diag
 412755; BE144306; Hs.179891; ESTs, Weekly similar to F4HJA-ht; angio; s.m.
 412811; H06382; Hs.349705; ESTs; lung; diag
 412817; AL037159; Hs.74819; proteasome (prosome, macropain; lung; s.m.
 412843; AF007655; Hs.74624; protein tyrosine phosphatase, ; pros; mAb
 412858; BE386745; Hs.74631; basigin (OK blood group); mela; mAb
 412926; AB79078; Hs.75061; macrophage myristoylated alan; mela; CTL+s.m.
 412939; AW411491; Hs.75069; eukaryotic translation elongat; mela; renal; diag
 412970; AB026438; Hs.177534; dual specificity phosphatase 1; breast; mela; s.m.
 412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glio; mAb
 413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag
 413011; AW088115; Hs.821; blytcan; lung; CTL+s.m.
 413045; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
 413095; AA494359; Hs.30715; potassium voltage-gated channel; panc; stom; renal; colon; mAb+s.m.
 413125; BE244588; Hs.75207; glyoxalase I; pros; s.m.
 413126; AW418203; Hs.174174; ESTs; angio; diag
 413128; AF292100; Hs.104613; RP42 homolog; lung; diag
 413132; NM_008823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.
 413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
 413163; Y00816; Hs.75218; protein tyrosine phosphatase, ; pros; mAb
 413171; AA318325; Hs.75219; tyrosinase-related protein 1; mela; mAb
 413190; AA151802; Hs.40368; adaptor-related protein complex; mela; diag
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis; esoph; cerv; diag
 413223; A1732182; Hs.191866; ESTs; lung; diag
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.
 413281; AA861271; Hs.22024; transcription factor BMAL2; lung; blad; headnk; panc; angio; diag
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble, ; pros; s.m.
 413335; A1613318; Hs.48442; ESTs; ovar; diag
 413364; BE536218; Hs.137516; fidgetin-like 1; lung; diag
 413372; H55532; Hs.345695; tubulin, alpha 2; test; diag
 413435; X51405; Hs.75360; carboxypeptidase E; pros; glio; panc; sarc; diag
 413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.
 413472; BE242870; Hs.75379; solute carrier family 1 (glut; glio; mAb
 413566; AW604451; Hs.381153; sprouty (Drosophila) homolog 4; sarc; CTL+s.m.

- 413573; A1733859; Hs.149089; ESTs; lung; diag
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
 413597; AW302885; Hs.117183; ESTs; pros; diag
 413623; AAB25721; Hs.246973; intron of Bicoid/D homolog 1; ovar; pros; diag
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
 413711; AW291766; Hs.75486; heat shock transcription factor; renal; diag
 413753; U17760; Hs.75517; laminin, beta 3 (nicotin (125kD); lung, blad, headnk, panc, cerv, esoph, colon; diag
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
 413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag
 413794; AF234532; Hs.61636; myosin X; meta; diag
 413804; T64682; gbcy48b02.r1 Stratagene liver; blad; diag
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag
 413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag
 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
 413842; M29363; Hs.856; Interferon, gamma; leuk; diag
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb
 413880; AJ660842; Hs.110915; interleukin 22 receptor; panc, colon; mAb+s.m.
 413924; AL119984; Hs.75616; seladin-1; pros, breast, ovar; diag
 413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 f1; blad, lung; CTL+s.m.
 413985; A1018666; Hs.75667; synaptophysin; glo, sarc; mAb
 414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, meta; diag
 414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
 414034; U89277; Hs.305985; early development regulator 1; test; CTL+s.m.
 414035; Y00630; Hs.75716; serine (or cysteine) proteinases; lung, cerv, headnk, blad; s.m.
 414053; BE391635; Hs.75725; transgelin 2; blad; diag
 414061; NM_000689; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 f1; pros; diag
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 family; pros, panc, sarc; s.m.
 414142; AW368397; Hs.334485; hemiscitin (fibulin 5); fibro, panc, sarc; diag
 414161; AA136106; Hs.184852; KIAA1553 protein; test; diag
 414166; AW88941; Hs.75789; N-myc downstream regulated; pros, renal; diag
 414217; AJ309298; Hs.279898; Homo sapiens cDNA: FLJ23165 f1; glo; diag
 414219; W20010; Hs.75823; ALL1-fused gene from chromosome; sarc; diag
 414221; AW450979; gh:ULI-H-B13-ala-a-12-D-ULI.s1 N; blad; diag
 414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.
 414259; W44633; Hs.301296; Integrin, beta-like 1 (with EG; panc; diag
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
 414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.
 414386; X00442; Hs.75980; hemoglobin; ovar; diag
 414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
 414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag
 414430; AJ348201; Hs.76118; ubiquitin carboxyl-terminal est; lung; s.m.
 414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 414477; U41835; Hs.76228; amplified in osteosarcoma; sarc; diag
 414505; AW161311; Hs.76294; CD63 antigen (melanoma 1 antig; meta; mAb
 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colon, stom, fibro; diag
 414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag
 414568; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 414576; H11257; Hs.375743; Homo sapiens clone IMAGE45183; renal; diag
 414595; AA641728; Hs.289015; hypothetical protein MGC4171; blad; diag
 414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
 414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag
 414732; AW410978; Hs.77152; minichromosome maintenance def; test, blad; diag
 414751; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.
 414776; AA155598; Hs.212839; hypothetical protein FLJ14195; angio; diag
 414786; AJ246482; Hs.243010; Homo sapiens cDNA FLJ14372 f1; angio; diag
 414799; AJ762416; Hs.77326; insulin-like growth factor bin; renal; diag
 414806; D14894; Hs.77329; phosphatidylserine synthase 1; lung; mAb
 414807; AJ738816; Hs.77346; hydroxyprostaglandin dehydrog; blad; s.m.
 414808; AA34659; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.
 414825; X06370; Hs.77432; epidermal growth factor recept; glo, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.
 414915; NM_002462; Hs.76391; myxovirus (influenza) resist; esoph; diag
 414918; AJ219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
 414945; BE076958; Hs.77667; lymphocyte antigen 6 complex; meta; mAb
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
 414998; NM_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb
 415003; M11437; Hs.77741; kinnogen; panc; diag
 415025; AW207091; Hs.72307; ESTs; blad; diag
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-CoA; lung, headnk; s.m.
 415178; D06503; Hs.48692; ESTs; blad; diag
 415214; A1445236; Hs.125124; EphB2; colon, stom; mAb
 415314; N88802; Hs.5422; glycoprotein M6B; meta; mAb
 415457; AW081710; Hs.7369; Homo sapiens testis specific A; fibro, ovar, uter; CTL+s.m.
 415511; A732617; Hs.182362; ESTs; blad, ovar, renal; diag
 415542; R13474; Hs.290263; ESTs, Weekly similar to 138022; blad; diag
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
 415752; BE314524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, meta; mAb
 415786; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 415787; H01463; Hs.93534; ESTs; pros; diag
 415819; AU077330; Hs.360791; transcription elongation factor; test; CTL+s.m.

- 415829; AW450198; Hs.163742; ESTs; test; diag
 416857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fls; lung; test; diag
 416910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
 416947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo; test; diag
 5 415989; A1267700; Hs.351201; ESTs; pros, ovar, blad, lung, headnk, panc, colon, sarc; diag
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros, fibro; mAb
 415999; AA172179; Hs.294029; ESTs; pros, ule; diag
 416018; AW138239; Hs.78977; proprotein convertase subtilis; colon, panc, lung; diag
 10 416030; H15261; Hs.21948; ESTs; breast, fibro; diag
 416055; BE267931; Hs.78996; proliferating cell nuclear ant; blad, lung, headnk, mela; CTL+s.m.
 416111; AA03813; Hs.79018; chromatin assembly factor 1, s; lung, stom; CTL+s.m.
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
 416201; AA467762; Hs.195161; ESTs; test; diag
 15 416208; AW291166; Hs.41295; ESTs, Weakly similar to MUC2_H; lung; diag
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag
 416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4269; pros, blad; diag
 416350; AF188625; Hs.189507; phospholipase A2, group I0; test, mela, fibro; diag
 416370; N90470; Hs.203697; CD38 antigen (p45); pros, glio; mAb+CTL
 20 416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag
 416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
 416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar, colon, stom; diag
 416498; U33632; Hs.79351; potassium channel, subfamily K; panc, stom, breast, ovar, colon; mAb
 416539; Y07909; Hs.79366; epithelial membrane protein 1; pros, headnk; diag
 25 416602; NM_005158; Hs.367695; Protein kinase C-binding prote; breast; diag
 416640; BE262478; Hs.13408; neuron-specific protein; mela; diag
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad, lung, headnk, cerv, panc, angio; diag
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactose; angio; s.m.
 30 416818; U77735; Hs.80205; plm-2 oncogene; lung, test; diag
 416881; N32620; Hs.141358; ESTs; mela; diag
 416929; N20535; Hs.43265; metastalin 1; mela; diag
 416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytotox; mela; s.m.
 417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.
 35 417070; Z19077; Hs.172004; tlin; sarc; diag
 417105; X60992; Hs.81226; CD6 antigen; fibro; mAb
 417116; AW952792; Hs.334612; small nuclear ribonucleoprotei; test; CTL+s.m.
 417124; BE122762; Hs.25338; ESTs; angio; diag
 417148; AA369896; Hs.374554; hypothetical protein FLJ14902; panc; diag
 417151; AA194055; Hs.293858; ESTs; blad; diag
 40 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros, sarc; diag
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
 417237; H06385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
 417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc, breast; diag
 417275; X63578; Hs.295448; parvalbumin; blad; diag
 45 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
 417308; H60720; Hs.81892; KIAA0101 gene product; lung, headnk, blad, cerv, angio, mela, sarc; diag
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
 417333; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 50 417356; D13168; Hs.82002; endothelin receptor type B; glio, mela; mAb
 417369; D50683; Hs.82028; transforming growth factor, be; fibro, angio; mAb
 417366; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad, headnk, panc, esoph, mela; diag
 417370; T26551; Hs.374466; tryptophanyl-tRNA synthetase; fibro, mela; diag
 417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 55 417400; AA653486; Hs.123072; RAB38, member RAS oncogene fam; pros; diag
 417407; AA923278; Hs.290805; ESTs, Weakly similar to protea; test, pros; s.m.
 417409; BE272506; Hs.82109; syndecan 1; blad; diag
 417412; X16898; Hs.82112; interleukin 1 receptor, type I; fibro, pros, panc; mAb
 417426; NM_002281; Hs.82124; laminin, beta 1; angio; diag
 60 417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
 417512; X76534; Hs.82228; glycoprotein (transmembrane) n; lung, mela, headnk, panc, breast; mAb
 417516; L24203; Hs.82237; alveola-angiogenesis group D-; lung, headnk, blad; diag
 417542; J04129; Hs.82269; progestagen-associated endomat; lung, mela; diag
 417592; AA204684; Hs.182437; ESTs, Weakly similar to I54383; test; diag
 65 417599; AA204688; Hs.62954; ESTs; blad, esoph; diag
 417621; AV654694; Hs.82316; interferon-induced, hepallle; esoph; diag
 417696; BE241824; Hs.82401; CD89 antigen (p60, early T-cell; pros; mAb
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
 417715; AW959587; Hs.86386; ESTs; blad, lung, headnk; diag
 70 417720; AA205625; Hs.208087; ESTs; blad, lung, esoph, headnk; diag
 417750; A1267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
 417777; A1823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.
 417791; AW965339; Hs.44269; ESTs; ovar, blad, lung, headnk; CTL+s.m.
 75 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EC; panc, fibro; diag
 417805; U38545; Hs.82587; phospholipase D1, phosphatidyl; angio; s.m.
 417831; H16423; Hs.82685; CD47 antigen (Rb-related antig; ovar; mAb
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fls; pros; diag
 417847; A1521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag
 417849; AW291587; Hs.82733; aldogen 2; angio, headnk; diag
 80 417874; BE616160; Hs.82829; protein tyrosine phosphatase, ; panc; mAb+s.m.
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion; mela; mAb
 417886; AA214584; ESTs; test, ovar; diag
 417900; BE250127; Hs.82908; CDC20 (cell division cycle 20; lung, stom, test, blad, headnk, cerv, esoph; CTL+s.m.
 417911; AA333387; Hs.82916; chaperonin containing TCF1, su; test; diag

- 417944; AU077198; Hs.82985; collagen, type V, alpha 2; sarc; diag
 417975; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb
 417976; BE665892; Hs.83077; interleukin 18 (interferon-gam; colon, stom, fibro; diag
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 fam1; lung, headnk, esoph; s.m.
 418036; Z37978; Hs.83337; latent transforming growth fac; angio; diag
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
 418067; A127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS; blad; s.m.
 418113; A1272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.
 418134; AA397769; Hs.86617; ESTs; test; diag
 418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
 418216; AA662240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag
 418245; AA088767; Hs.83883; transmembrana, prostate androg; panc; mAb+s.m.
 418283; S79895; Hs.83942; cathepsin K (pseudodysostosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhib; headnk, lung, blad; s.m.
 418336; NM_002522; Hs.84154; neuronal pentraxin 1; sarc; diag
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase; cerv, lung; s.m.
 418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb
 418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag
 418394; AF132818; Hs.84729; Kruppel-like factor 5 (intest); panc; CTL+s.m.
 418396; A1765805; Hs.26691; SLC2A12 Solute carrier family 1; pros; mAb
 418397; NM_001258; Hs.84746; chromosome condensation 1; lung; diag
 418398; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
 418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag
 418432; M14156; Hs.85112; insulin-like growth factor 1 (; pros, fibro; diag
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb
 418462; BE001596; Hs.85288; Integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
 418543; NM_005329; Hs.85862; hyaluronan synthase 3; blad, lung; mAb
 418576; AW968158; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.
 418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
 418655; AA226354; Hs.111240; ESTs; pros; diag
 418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
 418663; AK001100; Hs.41890; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
 418683; U90908; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.
 418686; Z36830; Hs.87268; annexin A8; blad, lung; diag
 418693; A1760878; Hs.87408; thrombospondin 1; angio, panc; diag
 418696; AW959433; Hs.326280; hypothetical protein FLJ12581; test; diag
 418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag
 418766; AA252254; Hs.226949; ESTs; test; diag
 418825; AA228851; Hs.22394; hypothetical protein FLJ10893; angio; diag
 418829; AA518531; Hs.55999; NK homeobox (Drosophila), fam1; pros; diag
 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-fam1; ovar, pros, breast, lung; diag
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.
 418886; AU076801; Hs.89436; cadherin 17, LI cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb
 418932; L34058; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
 418956; NM_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag
 418994; AA286520; Hs.89548; selectin E (endothelial adhe; pros, angio; mAb
 419038; AW134924; Hs.68280; ESTs; pros; diag
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2; ovar, renal, blad, lung; mAb
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
 419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
 419222; AD001528; Hs.89718; spermine synthase; pros; s.m.
 419223; X60111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag
 419261; X07876; Hs.89791; wingless-type MMTV Integration; panc; diag
 419284; AA877104; Hs.293872; ESTs, Weakly similar to ALUB_H; pros; diag
 419280; A128114; Hs.112885; spinal cord-derived growth fac; panc; diag
 419356; A1656168; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
 419440; AB020689; Hs.80418; KIAA0882 protein; breast; diag
 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
 419496; NM_006144; Hs.80708; granzyme A (granzyme 1, cyto; fibro; s.m.
 419519; A198719; Hs.176378; ESTs; mela; diag
 419551; AW582258; Hs.91011; anterior gradient 2 (Xenopus l; panc, pros, breast; diag
 419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.
 419568; AB026116; Hs.283078; hOAT4; renal; mAb
 419569; A1971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
 419628; H67546; Hs.49768; ESTs; mela, sarc; diag
 419667; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb
 419693; AA133749; Hs.301360; FYD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
 419721; NM_001650; Hs.315369; aquaporin 4; glio, lung, fibro; mAb
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mFNA; blad, headnk; diag
 419749; X73608; Hs.93029; sperolosteonectin, cwcv and ka; pros, panc, lung; diag
 419752; AA249573; Hs.152818; ESTs, Moderately similar to ZN; lung; diag

- 419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros; lung; diag
419870; AW403911; Hs.266175; phosphoprotein associated with; meta; diag
419875; AA853410; Hs.93557; proenkephalin; sarc; diag
5 419946; AB041035; Hs.93847; NM_016931: Homo sapiens NADPH o; angio; mAb
419956; AL137939; Hs.40096; cadherin 19, type 2; meta; mAb
419988; X04430; Hs.93913; interleukin 6 (interferon, bet; lung, panc, esoph; diag
419981; AA897581; Hs.128773; ESTs; angio; diag
10 420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
420062; AW411098; Hs.94785; TGF(beta)-induced transcript; test; CTL+s.m.
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptide; fibro; mAb
420154; AI033155; Hs.95420; G antigen family C 1 protein (s; pros, laic; CTL+s.m.
420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.
15 420208; BE276055; Hs.95972; silver (mouse homolog) like; meta; sarc; mAb
420209; AA256444; Hs.126485; hypothetical protein FLJ12604; angio; diag
420218; AW958037; Hs.381105; ribosomal protein L4; meta; pros; diag
420256; NM_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb
420256; U04722; Hs.76208; cadherin 5, type 2, VE-cadherin; angio; fibro; mAb
20 420267; N37030; Hs.173337; ESTs; meta; sarc; diag
420281; AI623693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; meta; diag
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339; meta; mAb
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide; fibro; mAb
25 420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
420347; AL033539; Hs.97124; Human DNA sequence from clone; test; diag
420360; U83171; Hs.97203; small inducible cytokine subfam; leuk; diag
420367; AA259090; Hs.257028; ESTs; test; diag
420378; AL137471; Hs.97265; protocadherin 18; sarc; mAb+s.m.
30 420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
420380; AA640891; Hs.102406; ESTs; lung; diag
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag
420462; AF050147; Hs.97932; chondromodulin 1 precursor; lung, EWS, sarc; mAb
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
35 420544; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag
420598; NM_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.
420633; NM_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endo; diag
420656; AA276098; Hs.187638; ESTs; fibro; diag
40 420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
420729; AW964897; Hs.290825; ESTs; pros; diag
420757; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 f5; test; diag
420783; AI659838; Hs.99323; lactin, galactoside-binding, s; lung, blad, headnk; diag
45 420789; AI670067; Hs.199882; ESTs; renal; diag
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
420880; AL048974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
420923; AF097021; Hs.273321; differentially expressed in her; blad, colon; diag
50 420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, meta; diag
420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.
421016; AA504583; Hs.101047; transcription factor 3 (E2A tm; test; CTL+s.m.
421044; AF081871; Hs.101302; Human DNA sequence from clone; panc; diag
421059; AI654133; Hs.355247; thyroid receptor interacting p; pros; mAb+s.m.
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-1; blad, uter; diag
55 421070; AA283185; Hs.19327; ESTs; blad; diag
421100; AW351838; Hs.124660; Homo sapiens cDNA: FLJ21763 f1; blad; diag
421133; AA814971; Hs.26410; ESTs; lung; diag
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 f5; BPH; diag
60 421155; H87879; Hs.102267; lysozyme; headnk, panc, renal, sarc; diag
421218; NM_000499; Hs.72912; cytochrome P450, subfamily I (s; blad, angio; diag
421233; AA209534; Hs.284243; tetraspan NET-6 protein; pros, breast, ovar; mAb
421241; X91817; Hs.102868; transketolase-like 1; test; s.m.
421302; T34462; Hs.103281; neuritin; uter, endo; diag
65 421305; BE397354; Hs.324830; diphtheria toxin resistance pro; ovar; diag
421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag
421341; AJ243212; Hs.279811; deleted in malignant brain tum; panc, lung; diag
421350; AW301608; Hs.278188; ESTs, Moderately similar to IS; test; diag
421373; AA808223; Hs.222088; ESTs; blad; diag
421433; AI829192; Hs.22380; ESTs; pros; diag
70 421451; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
421458; NM_003654; Hs.104576; carbohydrate (keratan sulfate; sarc; s.m.
421478; AI683243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
421502; AF111856; Hs.105039; solute carrier family 34 (sod); ovar, fibro; mAb
75 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, meta; CTL+s.m.
421535; AB002359; Hs.105478; phosphoribosylformylglycinamid; test; s.m.
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag
421566; NM_000399; Hs.1395; early growth response 2 (Krox; pros; CTL+s.m.
80 421579; NM_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb
421633; AF121860; Hs.106260; sorting nexin 10; meta; diag
421650; AA781795; Hs.343800; ESTs; meta; diag
421666; AL035260; Hs.1406; endothelin 3; meta; diag
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

- 421773; W69233; Hs.112457; ESTs; mela, esoph, sarc; diag
 421777; BE562088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
 421779; A1879169; Hs.108219; wingless-type MMTV integration; colon, ovar; diag
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.
 421814; L12350; Hs.108623; thrombospondin 2; panc; diag
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 421887; AW161450; Hs.109201; CGI-88 protein; pros; mAb
 421896; N62293; Hs.45107; ESTs; pros; diag
 421917; A8028943; Hs.109445; KIAA1020 protein; test; diag
 421920; BE551245; Hs.1436; gamma-aminobutyric acid (GABA); sarc; mAb
 421924; BE614514; Hs.109606; coronin, actin-binding protein; fibro; diag
 421946; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, mela; diag
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); fibro; diag
 421991; NM_014918; Hs.110486; KIAA0990 protein; panc; diag
 421996; AW583607; Hs.1460; glucagon; panc; diag
 422002; X70070; Hs.110642; neurolensin receptor 1 (high a; colon; mAb
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glio; mAb
 422087; X58968; Hs.111301; matrix metalloproteinase 2 (pe; sarc; diag
 422089; AA523472; Hs.103135; ESTs, Weakly similar to SFRA_1; pros; diag
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
 422095; A1868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
 422098; AA158022; Hs.111518; hypothetical protein; angio; CTL+s.m.
 422100; A1096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
 422110; A1378736; Hs.121555; secreted protein, acidic, cyst; panc; diag
 422119; A1277829; Hs.111882; KIAA0590 gene product; blad; diag
 422134; AW179019; Hs.112110; mitochondrial ribosomal prote; lung; diag
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
 422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor 1; blad; mAb+s.m.
 422188; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.
 422170; A1791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag
 422173; BE365828; Hs.250619; phorbollin-like protein MDS019; mela; diag
 422247; U18244; Hs.113602; solute carrier family 1 (high; blad; mAb
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar, headnk, blad, cerv, lung, panc, stom; mAb
 422309; U79745; Hs.114924; solute carrier family 16 (mono; mela; mAb+s.m.
 422311; AF073515; Hs.114943; cytokine receptor-like factor; lung, fibro; diag
 422355; AW403724; Hs.300697; coagulation factor VII (serum); fibro; diag
 422363; T55979; Hs.115474; replication factor C (activator; mela, colon; diag
 422398; A1476149; Hs.334488; hypothetical protein FLJ21992; fibro; CTL+s.m.
 422406; AF025441; Hs.116206; Ope-interacting protein 5; blad, lung; diag
 422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1; lung, headnk; s.m.
 422487; A1010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
 422532; AL008728; Hs.118128; protective protein for beta-ga; renal, mela; s.m.
 422565; BE269036; Hs.118400; singed (Drosophila)-like (sea; panc, test, mela; diag
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin); panc; mAb+s.m.
 422596; AF063611; Hs.118833; 2'-5'-oligoadenylate synthetase; esoph, mela; s.m.
 422603; BE242587; Hs.118651; hematopoietically expressed hox; angio; CTL+s.m.
 422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.
 422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag
 422689; AW566665; Hs.299797; gbrRC3-CT0297-290100-013-d03 C; test; diag
 422728; U11690; Hs.1572; facio-genital dysplasia (Aarskog; test; diag
 422728; AW937826; Hs.103282; MAD (mothers against decapentap; pros; diag
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
 422835; BE218705; Hs.124378; metallothionein-like 5, testis; breast; diag
 422871; AL031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
 422887; A1751848; Hs.48215; ESTs; sarc; CTL+s.m.
 422836; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
 422963; M79141; Hs.13234; ESTs; lung, panc; diag
 422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase; blad, headnk, mela; mAb+diag
 423052; M28214; Hs.123072; RAB38, member RAS oncogene fam; pros; diag
 423169; M59371; Hs.171696; EphA2; colon, ovar; mAb
 423195; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.
 423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
 423201; NM_000163; Hs.126180; growth hormone receptor; pros; mAb
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (a; lung, esoph; diag
 423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
 423354; AB011130; Hs.127438; calcium channel, voltage-depend; test, fibro; mAb
 423387; A1012074; Hs.348500; vasoactive intestinal peptide; pros; mAb
 423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb
 423412; AF109300; Hs.361615; prostate cancer associated pro; pros; diag
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glio; mAb+CTL
 423445; NM_014324; Hs.128748; alpha-methylacyl-CoA racemase; pros; s.m.
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
 423458; A1204212; Hs.351113; ESTs; test; CTL+s.m.
 423511; AF036328; Hs.129715; gonadotropin-releasing hormone; lung; diag
 423515; AA327017; Hs.176594; ESTs; ovar; diag
 423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag
 423575; C18863; Hs.163443; Intron of perostin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047826; Hs.129887; cadherin 19, type 2; mel; mAb
 423642; AYW452850; Hs.157148; hypothetical protein MGC13204; lung; diag
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc); lung; diag
 423685; BE350484; Hs.49753; uveal autoantigen with coiled; panc, uter, colon; CTL+s.m.
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
 423739; AA398155; Hs.57600; ESTs; breast, ovar, panc; diag
 423761; NM_006194; Hs.132576; paired box gene 9; headnk; CTL+s.m.
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
 423778; Y09287; Hs.132821; flavin containing monooxygenase; fibro; s.m.
 423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glio; diag
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test, esoph; diag
 423798; AF047033; Hs.132904; soluble carrier family 4, sodli; angio; mAb
 423799; AW028300; Hs.132906; 19A24 protein; mel; mAb
 423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
 423887; AL080207; Hs.134588; DKFZP434G232 protein; headnk, lung; diag
 423899; NM_001427; Hs.134989; engrailed homolog 2; mel; CTL+s.m.
 423905; AW679960; Hs.135150; lung type-I cell membrane-assoc; test; mAb
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, ma; test; diag
 423934; U89895; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag
 424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
 424036; AA770688; Hs.348495; H2A histone family, member L; panc, ovar; CTL+s.m.
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb
 424078; AB008625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); test; s.m.
 424088; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
 424125; M31668; Hs.1735; Inhibin, beta B (activin AB b; ovar, pros; diag
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
 424153; AA451737; Hs.141496; MAGE-like 2; mel; CTL+s.m.
 424165; AW562904; Hs.142256; islet amyloid polypeptide; panc; mAb
 424212; NM_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); mel, fibro; diag
 424244; AV647184; Hs.143801; hypothetical protein hCLA-iso; blad; diag
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
 424284; D80400; Hs.239388; Human DNA sequence from clone; blad; mAb
 424308; AW875531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
 424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag
 424332; AA338918; Hs.101615; ESTs; pros; diag
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
 424343; AW956360; Hs.4748; adenylate cyclase activating p; glio, ovar, uter; mAb
 424384; AW383228; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
 424399; AF056887; Hs.348419; A1905667:IL-BT085-180190-019 B; breast, uter, headnk; diag
 424420; BE514743; Hs.146886; prostaglandin E synthase; lung, blad; s.m.
 424440; AA304743; Hs.133208; ESTs; sarc; diag
 424441; X14850; Hs.147097; H2A histone family, member X; lung; diag
 424450; AL137528; Hs.147472; dynein intermediate chain 2; fibro; diag
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
 424527; AW138556; Hs.334873; ESTs, Weakly similar to 154374; fibro; diag
 424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.
 424581; M62062; Hs.150917; catenin (cadherin-associated p; glio, ovar, uter; mAb+s.m.
 424588; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
 424628; M80858; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fls; glio; diag
 424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 424704; A1263293; Hs.152098; cytochrome P450, subfamily II; renal; s.m.
 424711; NM_005795; Hs.152175; catatonin receptor-like; angio; mAb
 424717; H03754; Hs.152213; wingless-type MMTV Integration; blad, lung, headnk; diag
 424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag
 424806; AA382523; Hs.105689; MSTP031 protein; angio; mAb
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fls; lung, blad, ovar, headnk, esoph, cerv, uter; diag
 424846; AU077324; Hs.1832; neuropeptide Y; pros; diag
 424897; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 424902; NM_003866; Hs.153687; inositol polyphosphate-4-phosp; panc, leuk, mel; CTL+s.m.
 424954; NM_000546; Hs.1848; tumor protein p53 (Li-Fraumeni; mel, colon; CTL+s.m.
 424971; AA479005; Hs.154036; tumor suppressing subtransfer; panc, mel; CTL+s.m.
 424998; U58515; Hs.154138; chitinase 3-like 2; glio; diag
 425023; AW956889; Hs.154210; EDG-1 (endothelial different); angio; mAb
 425048; H05488; Hs.164502; ESTs; lung, blad; diag
 425057; AA826434; Hs.1619; achaete-scute complex (Drosoph; glio, lung; CTL+s.m.
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glio, mel; diag
 425164; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
 425200; BE255203.comp; Hs.155101; ATP synthase, H transporting; ; panc; s.m.
 425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
 425211; M18667; Hs.1867; progastricin (pepsinogen C); fibro, esoph, pros; diag
 425234; AW152226; Hs.165909; ESTs, Weakly similar to 138022; lung, angio, blad, mel; diag
 425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 fl; angio; diag
 425237; U07695; Hs.155227; EphB4; test; mAb
 425245; A1751768; Hs.165314; KIAA0095 gene product; lung; diag
 425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 425262; D87119; Hs.155418; GS3955 protein; mel, renal; CTL+s.m.
 425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

- 425289; AW139342; Hs.155530; Interferon, gamma-inducible p; mela; CTL+s.m.
 425308; M97639; Hs.155586; receptor tyrosine kinase-like; pros; sarc; mAb
 425367; BE271188; Hs.155975; protein tyrosine phosphatase; fibro; diag
 425371; D49441; Hs.155981; mesothelin; ovar; lung; fibro; mAb
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha; lung, blad, panc, angio, test, mela, esoph; CTL+s.m.
 425427; AJ652662; Hs.317432; branched chain aminotransferase; test; s.m.
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
 425465; L18964; Hs.1904; protein kinase C, α ; ovar; pros; colon; s.m.
 425525; AA358883; Hs.23871; ESTs; sarc; diag
 425545; N98529; Hs.158295; Homo sapiens, clone MGC12401; sarc; diag
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 f; fibro; CTL+s.m.
 425572; AB011076; Hs.158307; undifferentiated embryonic cell; test; CTL+s.m.
 425601; AW623485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.
 425606; U52112; Hs.158331; renin-binding protein; mela; diag
 425628; NM_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
 425679; X05897; Hs.159177; lipase, gastric; esoph; s.m.
 425892; D90041; Hs.155956; N-acetyltransferase 1 (aryl); breast; s.m.
 425895; NM_005401; Hs.159238; protein tyrosine phosphatase; lung; mAb+s.m.
 425709; AA383076; Hs.158274; outer dense fibre of sperm tail; test; diag
 425710; AF030880; Hs.159275; solute carrier family, member; pros; mAb
 425722; AJ669076; Hs.97031; hypothetical protein MGC13047; mela; diag
 425726; AF085808; Hs.159330; uropodkin 3; pros; blad; diag
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA; test; diag
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort); test; diag
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
 425921; NM_007231; Hs.162211; solute carrier family 6 (neuro; stom, panc; mAb
 425976; C75094; Hs.334514; NG22 protein; pros; ovar; mAb
 426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
 426050; AF017307; Hs.166096; E74-like factor 3 (ets domain); ovar, blad, stom; CTL+s.m.
 426059; BE292842; Hs.166120; Interferon regulatory factor 7; esoph, cerv; CTL+s.m.
 426067; AW664691; Hs.97053; ESTs; lung; diag
 426088; AF038007; Hs.166198; ATPase, Class I, type 8B, memb; blad, lung; mAb
 426094; AF034611; Hs.166206; cubilin (intrinsic factor-cofra; renal; diag
 426116; AA868728; Hs.144694; ESTs; fibro; diag
 426125; X87241; Hs.166894; FAT tumor suppressor (Drosophi; colon, stom, panc, pros, renal, fibro, cerv; mAb
 426156; BE244637; Hs.167382; nutritive peptide receptor A; ovar; mAb
 426158; NM_001892; Hs.199067; v-erb-b2 avian erythroblast; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; diag
 426172; AA371307; Hs.125056; ESTs; pros; diag
 426174; AA547959; Hs.115838; Homo sapiens similar to Echinoc; breast, pros, fibro; diag
 426212; S71824; Hs.167988; neural cell adhesion molecule; glio; mAb
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glio; diag
 426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb
 426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb
 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb
 426312; AF026938; Hs.181874; Interferon-induced protein wit; esoph, mela; diag
 426320; W47595; Hs.189300; transforming growth factor, β ; ovar, pros, blad, panc; diag
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
 426363; M58524; Hs.2025; transforming growth factor, β ; pros; diag
 426370; R58288; Hs.281706; sortilin 1; sarc; diag
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
 426440; BE382766; Hs.169902; solute carrier family 2 (facil; lung, panc, ovar, blad, headnk, esoph; mAb
 426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag
 426470; AA526794; Hs.128644; ESTs; mela; diag
 426471; M22440; Hs.170009; transforming growth factor, α ; headnk, renal, panc; diag
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.
 426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mela; mAb
 426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag
 426534; U58086; Hs.2051; testis specific protein, Y-In; test; CTL+s.m.
 426535; AJ077012; Hs.170279; ESTs, Weekly similar to ubiquit; angio; diag
 426556; NM_000372; Hs.2053; tyrosinase (oculocutaneous alb; mela, sarc; mAb
 426559; AB001914; Hs.170414; paired basic amino acid cleav; hepC, breast, ovar, renal; diag
 426575; M74825; Hs.170808; glutamate decarboxylase 2 (pan; panc; s.m.
 426627; AF012359; Hs.195685; ESTs; test; diag
 426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.
 426682; AV660038; Hs.2056; UDP glycosyltransferase 1 fam1; blad, lung; s.m.
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 f; angio; mAb
 426721; AA383588; Hs.288545; ESTs, Weekly similar to T28012; fibro; diag
 426728; AA488915; Hs.171955; trophoblast associated protein 1; test; diag
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
 426752; X69490; Hs.172004; tlin; sarc; diag
 426759; AJ590401; Hs.21213; ESTs; mela; diag
 426793; X89887; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.
 426828; NM_000020; Hs.172670; activin A receptor type II-like; angio; mAb
 426868; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
 426897; AW976570; Hs.97387; ESTs; lung; diag
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
 426936; NM_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.
 426966; AJ493134; Hs.349204; sclerostin; lung; diag
 426968; U07618; Hs.173034; amphiphysin (Shiff-Mann syndro; blad; mAb+CTL
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 f; ovar, sarc; diag
 427060; AW068287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

- 427099; AB032853; Hs.173560; odd Oz/ten-m homolog 2 (Drosop; headnk, esoph; diag
427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb
427244; AA402400; Hs.178045; ESTs; esoph; diag
5 427260; AA663848; ; gb:aa70b06.s1 Stratagene schiz; lung; diag
427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb
427290; AA400485; ; ESTs; test; diag
427318; AF185081; Hs.175783; zinc transporter; pros; mAb
427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
10 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin); ovar; mAb
427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag
427427; AF077345; Hs.177936; lectin, superfamily member 1 f; breast; diag
427441; AA412805; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
15 427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb
427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfate; sarc; diag
427486; AA974433; Hs.362432; fibroblast growth factor 4 (he; test; diag
427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
427515; T79526; Hs.179516; integral type I protein; pros; diag
20 427521; AW973352; ; ESTs; test; diag
427528; AU077143; Hs.179565; minichromosome maintenance def; meta; CTL+s.m.
427535; R29543; Hs.2184; pro-platelet basic protein (in; fibro; diag
427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
427560; BE242818; Hs.311609; nuclear RNA helicase, DECD var; meta; CTL+s.m.
25 427557; NM_002659; Hs.179557; plasminogen activator, urokinase; panc, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb
427576; A1591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
427583; M82962; Hs.179704; meprin A, alpha (PABA peptide; colon; mAb
427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, sarc; diag
30 427616; BE410107; Hs.179817; CGI-82 protein, PSDR1; pros; diag
427634; A1399745; Hs.18449; hypothetical protein MGC10820; meta, sarc; diag
427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20663 f1s; sarc; diag
427666; A1791495; Hs.180142; calmodulin-like skin protein f; breast, cerv, blad, lung, headnk, esoph; diag
427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 f1s; test; diag
35 427668; AA298760; Hs.180181; hypothetical protein FLJ14904; lung, test; diag
427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.
427698; AW972594; Hs.335498; ESTs; fibro; CTL+s.m.
427701; AA411101; Hs.243886; nuclear autoantigenic sperm pr; lung; mAb+CTL
427716; BE245274; Hs.180428; KIAA1181 protein; pros; diag
40 427719; A1393122; Hs.134726; ESTs; test, blad; diag
427730; AW250549; Hs.180577; granulin; meta; diag
427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
427811; M31057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.
45 427897; NM_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag
427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
427961; AW293165; Hs.143134; ESTs; lung, sarc; diag
50 428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; meta; diag
428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 f1; lung; diag
428046; AW812795; Hs.337534; ESTs, Moderately similar to l3; lung, colon; diag
428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
428067; AA100673; Hs.182421; troponin C2, fast; sarc; CTL+s.m.
55 428141; D60402; Hs.182611; solute carrier family 11 (prot; glio; mAb
428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
428169; A1928984; Hs.182793; golgi phosphoprotein 2; pros; diag
428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, sarc; CTL+s.m.
428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
60 428208; AB020843; Hs.183008; KIAA0836 protein; angio; mAb
428221; U96761; Hs.183076; ATPase, Ca transporting, card; sarc; s.m.
428227; AA321648; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, meta, esoph, hepC; diag
428248; A1126772; Hs.40479; ESTs; sarc; diag
65 428293; BE250944; Hs.183558; solute carrier family 1 (neut; pros; mAb
428305; AA446628; Hs.2799; cartilage linking protein 1; sarc; diag
428320; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
428336; AA503115; Hs.183752; microseminoprotein, beta; pros; diag
428366; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag
70 428398; A1249368; Hs.98558; ESTs; pros, breast; diag
428405; Y00762; Hs.2266; cholinergic receptor, nicotinic; esoph, sarc; mAb
428423; AU076517; Hs.184276; solute carrier family 9 (acid; ovar; CTL+s.m.
428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag
428467; AK002121; Hs.184465; hypothetical protein FLJ11269; fibro; mAb
428471; X57348; Hs.184510; stratifin; lung, headnk, colon, panc; diag
75 428648; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.
428651; AF196478; Hs.188401; annexin A10; blad, stom, panc; diag
428667; A1375550; Hs.346868; nucleolar protein p40; homolog; fibro, utar; diag
428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag
428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
80 428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
428784; Y12851; Hs.193470; purinergic receptor P2X, ligand; glio, meta; mAb
428800; M57627; Hs.193717; interleukin 10; fibro; diag
428801; AW277121; Hs.254881; ESTs; pros; diag
428804; AK000713; Hs.193736; hypothetical protein FLJ20706; meta; diag

- 428810; AF068236; Hs.193788; nitric oxide synthase 2A (indu; lung; s.m.
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
 428824; W23624; Hs.173059; ESTs; panc; diag
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZNF; panc, uter; diag
 428841; A1418430; Hs.104935; ESTs; renal; diag
 428848; NM_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag
 428862; NM_000346; Hs.2318; SRY (sex determining region Y); pros, sarc; CTL+s.m.
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
 428928; BE408838; Hs.194657; cadherin 1, type 1, E-cadherin; pros, breast, stom, blad; mAb
 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
 428957; NM_003881; Hs.194679; WNT1 inducible signalling pathw; cerv; diag
 428959; AF100779; Hs.194680; WNT1 inducible signalling pathw; sarc; diag
 428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_H; sarc; diag
 429002; AW248439; Hs.2340; junction plakoglobin; blad; CTL+s.m.
 429010; Y18198; Hs.194725; one cut domain, family member; panc; diag
 429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
 429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag
 429065; A1753247; Hs.29843; Homo sapiens cDNA FLJ13103 fic; lung; diag
 429083; Y09397; Hs.227817; BCL2-related protein A1; mela; diag
 429113; D28235; Hs.196384; prostaglandin-endoperoxide syn; angio, blad, stom; s.m.
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
 429150; AF120103; Hs.197368; smoothened (Drosophila) homolog; ovar; mAb
 429163; AA884766; gb:am20a10.a1 Soares_NFL_T_GBC; pros; diag
 429170; NM_001394; Hs.2358; dual specificity phosphatase 4; breast, panc, stom, lung, mela; s.m.
 429201; X03178; Hs.198246; group-specific component (vita; panc; diag
 429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag
 429228; A1553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
 429259; AA420450; Hs.380088; Plakophilin; lung, headnk; diag
 429290; AF203032; Hs.198760; neurofilament, heavy polypept; pros; CTL+s.m.
 429298; A1820463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag
 429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3; sarc; mAb
 429345; R11141; Hs.199695; hypothetical protein; blad; diag
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (m; headnk, breast, cerv, ovar, blad, lung, esoph, mela, sarc; mAb
 429413; NM_014058; Hs.201877; DESC1 protein; lung, blad; diag
 429415; NM_002593; Hs.202097; procollagen C-endopeptidase ent; sarc; diag
 429423; A1016712; Hs.380983; Integrin, beta 1 (fibronectin; angio; mAb
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fam; breast, pros, ovar; diag
 429466; M85835; Hs.12827; ESTs; glo, uter; CTL+s.m.
 429468; M54590; Hs.380791; glycine dehydrogenase (decarbo; test; s.m.
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto; lung, glo, headnk, mela, sarc; diag
 429504; X99133; Hs.204238; Epocalin 2 (oncogene 24p3) (N; ovar, lung, blad; diag
 429505; AW820035; Hs.278678; a disintegrin and metalloprote; colon, leuk; mAb
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
 429583; BE618413; Hs.2437; eukaryotic translation Initiat; lung; diag
 429596; T73610; Hs.209153; angiopeletin-like 3; hepC; CTL+s.m.
 429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb
 429609; AF002246; Hs.210863; cell adhesion molecule with ho; ovar, mela; diag
 429612; AF062649; Hs.252687; pituitary tumor-transforming 1; lung, blad, headnk; diag
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pros; s.m.
 429653; M68874; Hs.211587; phospholipase A2, group IVA (c; angio, lung; s.m.
 429664; L20433; Hs.211588; POU domain, class 4, transcrip; sarc; CTL+s.m.
 429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb
 429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
 429769; NM_004917; Hs.218366; kallikrein 4 (prolase, enamel; pros; s.m.
 429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb
 429823; AA459443; Hs.181400; ESTs; sarc; diag
 429859; NM_007050; Hs.225952; protein tyrosine phosphatase; breast; mAb+s.m.
 429916; AW873986; Hs.119383; ESTs; pros, glo; diag
 429921; AA626911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
 429983; W92820; Hs.260855; ESTs; blad; diag
 429986; AF092047; Hs.227277; elne oculis homeobox (Drosophi; lung; CTL+s.m.
 430014; H59354; Hs.374303; actinin, alpha 4; renal; diag
 430016; NM_004738; Hs.227656; xenotropic and polytropic retr; ovar; mAb
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
 430056; X97548; Hs.228099; KRAB-associated protein 1; test; CTL+s.m.
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
 430144; A1732722; Hs.98927; ERGL protein; ERGIC-53-like pr; pros; diag
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
 430154; AW583058; Hs.234726; serine (or cysteine) proteinase; pros; diag
 430157; BE348706; Hs.278543; ESTs; blad; diag
 430168; AW988343; Hs.145582; DKFZp434i1735 protein; blad; diag
 430223; NM_002514; Hs.235835; nephroblastoma overexpressed g; mela; diag
 430228; BE245662; Hs.2551; adrenergic, beta-2-, receptor; pros; mAb
 430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glo; diag
 430252; A1638774; Hs.106328; testes development-related NYD; test; CTL+s.m.
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
 430258; BE550182; Hs.375142; RalGEF-like protein 3, mouse h; ovar; CTL+s.m.

- 430280; AA361256; Hs.237858; Interleukin 7 receptor; mala; lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_H; test; diag
 430294; A1538226; Hs.32976; guanine nucleotide binding pro; pros; diag
 430337; M36707; Hs.238600; calmodulin-like 3; lung; diag
 430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag
 430378; Z29572; Hs.2558; tumor necrosis factor receptor; lung, fibro, breast headnk, blad, breast, colon, stom; diag
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag
 430407; H23551; Hs.30974; ESTs; panc; diag
 430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
 430454; AW469011; Hs.105635; ESTs; lung; diag
 430476; AAA47465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag
 430487; D87742; Hs.241552; KIAA0268 protein; pros; diag
 430491; AL109791; Hs.241559; Homo sapiens mRNA full length; ovar; diag
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag
 430508; AJ015436; Hs.104637; ESTs; lung; mAb+s.m.
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
 430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 f; mala; mAb
 430583; AA481269; Hs.348628; ATP-binding cassette, sub-fam; lung; diag
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mala; diag
 430634; A1860651; Hs.26685; calcyphosine; ovar; diag
 430637; BE160081; Hs.256290; S100 calcium-binding protein A; mala; diag
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_H; test; diag
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope prote; test; diag
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
 430678; A458174; Hs.192855; ESTs; lung; diag
 430688; NM_001942; Hs.2633; desmoglein 1; lung, headnk, mala; mAb
 430691; C14187; Hs.157208; aristaeless-related homeobox pr; EWS, ovar, panc; diag
 430704; AW813091; Hs.335799; ESTs; stom; diag
 430770; AA765694; Hs.123296; ESTs; mala; diag
 430832; AJ073913; Hs.100886; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
 430838; M46654; Hs.169395; hypothetical protein FLJ12015; mala; CTL+s.m.
 430850; X54232; Hs.2689; glypican 1; glo, lung, cerv, blad, esoph; mAb
 430885; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb
 431009; BE149762; Hs.48956; gap junction protein, beta 6 f; lung, blad, headnk, esoph; mAb
 431053; S40369; Hs.249141; Glutamate receptor subunit; glo; mAb
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
 431089; BE041396; Hs.374629; ESTs, Weakly similar to unknown; blad, lung, pros, angio, fibro; diag
 431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cl; pros; CTL+s.m.
 431103; M57399; Hs.44; pleiotrophin (heparin binding; sarc, mala; diag
 431124; AF284221; Hs.69506; doublesex and snab-3 related t; lung; CTL+s.m.
 431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH_MGC_7 Homo s; pros; mAb
 431164; AA483650; Hs.54367; thyroid transcription factor 1; fibro; CTL+s.m.
 431183; NM_006855; Hs.250696; KDE1 (Lys-Asp-Glu-Leu) endopla; mala, pros, panc, colon, stom; mAb
 431211; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk, esoph; mAb
 431217; NM_013427; Hs.250830; Rho GTPase activating protein; pros; CTL+s.m.
 431221; AAA49015; Hs.286145; SRB7 (suppressor of RNA polym; lung; CTL+s.m.
 431222; X56777; Hs.273780; zona pellucida glycoprotein 3A; pros; diag
 431250; BE264648; Hs.251377; taxol resistance associated ga; esoph; diag
 431322; AW970622; Hs.376526; gb:EST382704 MAGE resequences; blad, ovar, uter; diag
 431347; A113461; Hs.251684; Insulin-like growth factor 2 f; blad; mAb+diag
 431354; BE046856; Hs.251673; DNA (cytosine-5)-methyltransf; test; CTL+s.m.
 431360; NM_000427; Hs.251680; koricin; mala, sarc; diag
 431362; A1874223; Hs.293560; ESTs; angio; diag
 431369; BE184455; Hs.251754; secretory leukocyte protease i; ovar, blad; diag
 431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 f; lung; diag
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
 431448; AL137517; Hs.308204; hypothetical protein DKFZp5640; blad; mAb
 431457; NM_012211; Hs.256297; integrin, alpha 11; headnk; mAb
 431474; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 431494; AA891355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
 431548; A1834273; Hs.9711; novel protein; lung, angio, pros; diag
 431553; X78075; Hs.2789; cartilage linking protein 1; sarc; diag
 431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon; mAb
 431674; AA088901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
 431728; NM_007351; Hs.268107; multimerin; angio; diag
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
 431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme; mala; mAb
 431870; AW448902; Hs.105500; ESTs; renal; diag
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb
 431938; AA838471; Hs.54431; specific granule protein (28 k; panc; diag
 431939; AW008081; Hs.231994; ESTs; renal, colon; diag
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 f; cerv, glo; diag
 431989; AW972870; Hs.291069; ESTs; ovar; diag
 431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glo; s.m.
 432004; BE018302; Hs.2894; placental growth factor, vascu; renal; diag
 432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 432117; AL036195; Hs.2909; prolamine 1; test; CTL+s.m.
 432126; AA127221; Hs.66; ESTs; angio; diag
 432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.
 432189; AA527941; ; gb.nh30c04.s1 NCI_CGAP_Pr3 Hom; pros; diag
 432199; AI693816; Hs.127179; cryptic gene; panc; diag
 432210; AI567421; Hs.273330; Homo sapiens, clone IMAGE:3644; ovar, lung, blad; diag
 432222; AI204996; ; gb.an03c03.x1 Stratagene schz; angio, blad, fibro; diag
 432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (c); blad, lung, headnk, esoph, sarc; s.m.
 432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
 432305; M62402; Hs.274313; insulin-like growth factor bnc; cerv; diag
 432374; W68816; Hs.301885; Homo sapiens cDNA FLJ11346 fis; cerv, lung, fibro, pros; diag
 432407; AA221036; ; gb.z03112.r1 Stratagene NT2 n; lung, test; colon; diag
 432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag
 432435; BE218866; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear f; blad, fibro, pros; diag
 432473; AI202703; Hs.152414; ESTs; pros; diag
 432481; AW451645; Hs.151504; Intron of collagen, type XI, a; sarc; diag
 432512; NM_003284; Hs.3017; transition protein 1 (during h; test; CTL+s.m.
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUA; fibro, ovar, uter; CTL+s.m.
 432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag
 432542; AW083920; Hs.16098; claudin 2; colon, panc; diag
 432589; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
 432616; AA557191; Hs.65028; ESTs, Weakly similar to I54374; pros; diag
 432621; AI298501; Hs.21192; ESTs, Weakly similar to T48428; pros; mAb
 432629; AW606549; Hs.280658; ESTs; ovar; diag
 432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung; mAb+s.m.
 432666; AW204089; Hs.351118; ESTs, Weakly similar to unname; test; diag
 432706; NM_013230; Hs.286124; CD24 antigen (small cell lung; colon, ovar, pros; mAb+CTL
 432730; AI066520; Hs.131358; ESTs; test; diag
 432731; F31176; Hs.287820; fibronectin 1; panc, fibro; diag
 432786; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 f; lung, ovar; CTL+s.m.
 432800; BE391046; Hs.278962; AIM-1 protein; melo, pros; mAb
 432842; AW674083; Hs.334822; hypothetical protein MGC4486; blad, lung, headnk; CTL+s.m.
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); telo; mAb
 432856; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
 432867; AW016936; Hs.233364; ESTs; stom, colon; diag
 432878; BE386490; Hs.279683; Pcdn; melo; CTL+s.m.
 432887; AI926047; Hs.162859; AK056805; Homo sapiens cDNA FL; pros; diag
 432936; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 432966; AA650114; Hs.325198; ESTs; pros; diag
 433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, y; melo; diag
 433013; AI697890; Hs.127337; axin 2 (conductin, axl); colon; CTL+s.m.
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 433088; NM_006456; Hs.288215; sialyltransferase; breast, ovar, melo; s.m.
 433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 fis; blad; diag
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex; ; blad, lung, headnk, cerv; mAb
 433147; AF091434; Hs.43080; platelet derived growth factor; ovar, panc, fibro; diag
 433159; AB035898; Hs.150567; kinesin-like protein 2; ovar, uter, colon, blad; diag
 433170; AB037616; Hs.8982; KIAA1395; angio; diag
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
 433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.
 433258; AI806626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
 433286; AW975944; Hs.237396; ESTs; breast, pros; diag
 433299; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
 433323; AA805132; Hs.159142; ESTs; pros; diag
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.
 433336; AF017986; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag
 433364; AI075407; Hs.296083; ESTs, Moderately similar to IS; melo; diag
 433365; AF026944; Hs.293797; ESTs; blad; diag
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
 433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
 433404; T32982; Hs.352670; Homo sapiens cDNA FLJ32064 fis; pros; diag
 433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, gilo, colon; s.m.
 433444; AW975324; Hs.129816; ESTs; pros; diag
 433458; AA508353; Hs.105914; relaxin 1 (H1); pros; diag
 433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.
 433486; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag
 433576; BE080715; Hs.161091; ESTs; melo; diag
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene; colon; diag
 433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb
 433701; AW445023; Hs.15155; ESTs; test; diag
 433724; AI827749; Hs.144924; serine/threonine protein kinase; test; CTL+s.m.
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM; pros, ovar; diag
 433800; AI034361; Hs.135150; lung type-I cell membrane-assoc; gilo, lung, test; mAb
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
 434011; AW953437; Hs.6486; clone FLB5214; pros; diag
 434105; AW952124; Hs.13094; prekerline associated thrombo; lung; diag
 434217; AW014795; Hs.23349; ESTs; angio; diag
 434262; AF121858; Hs.12169; sorting nexin 8; melo; CTL+s.m.
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

- 5 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis; test; diag
434340; A1193043; Hs.353146; ESTs, Weakly similar to T17228; lung; diag
434360; AW015415; Hs.127780; ESTs; lung; diag
434370; AF130888; Hs.56346; ectodysplasin 1, anhidrotic re; colon, stom; diag
434377; AW137148; Hs.306583; intron of perostin (OSF-2os); headnk; diag
434398; AA121098; Hs.3838; serum-inducible kinase (SNK); angio, breast; CTL+s.m.
434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
10 434414; AF798376; ; gb:34507.x1 NCL CGAP_Ov23 Ho; lung, test, colon; diag
434423; NM_005768; Hs.3844; LIM domain only 4; panc; diag
434449; AW953484; Hs.3849; hypothetical protein FLJ22041; sarc; diag
434487; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.
434596; T59538; ; gb:565g12.s1 Stralagene ovary; angio; s.m.
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.
15 434609; R76593; ; gb:560c11.r1 Soares placenta; pros; diag
434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
434649; AA788254; Hs.165390; ESTs, Highly similar to A40350; test; diag
434666; AA642126; Hs.74502; gb:mr60c01.s1 NCL CGAP_Lym3 Ho; panc; diag
434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
20 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis; panc; diag
434826; AF155661; Hs.22265; pyruvate dehydrogenase phospho; mela; s.m.
434846; AW295389; Hs.118768; ESTs; angio; diag
434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; lung, blad; mAb
434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
25 434973; AW449285; Hs.313636; EST; pros; diag
435045; BE297155; Hs.143698; ESTs; test; diag
435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
435066; BE281750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
435080; A1831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
30 435094; A1560129; Hs.289008; EST; ovar, cerv; diag
435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, mela; CTL+s.m.
435140; AA668123; Hs.134170; ESTs; fibro; diag
435159; AA668879; Hs.118649; ESTs; lung; diag
435206; A1432364; Hs.160594; ESTs; test; diag
35 435243; AW292886; Hs.348932; hypothetical protein dJ434014; cerv, headnk; diag
435292; N20514; Hs.172965; ESTs; mela; diag
435299; A1745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag
435479; AF197137; Hs.155101; ATP synthase, H transporting, ; pros; s.m.
435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
40 435563; AF210317; Hs.95497; solute carrier family 2 (facil; blad; mAb+s.m.
435576; AF213457; Hs.44234; triggering receptor expressed ; fibro; mAb+s.m.
435602; AF217516; Hs.283532; uncharacterized bone marrow pr; test; diag
435615; Y15066; Hs.4975; potassium voltage-gated channel; glio; mAb
435652; N32388; Hs.334370; uncharacterized hypothalamus pr; panc; diag
45 435793; A5037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag
435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
435876; AW1812586; Hs.160271; G protein-coupled receptor 48; pros; mAb
435897; AF269223; Hs.128322; L-complex 11 (a murine top hom; test; diag
435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
50 435918; AF263538; Hs.88232; growth differentiation factor ; test; diag
435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
436032; AA150787; Hs.109276; latexin protein; panc, angio; diag
436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag
436120; A1248193; Hs.118880; ESTs; fibro; diag
55 436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
436246; AW450963; Hs.118981; ESTs; blad; diag
436251; BE515085; Hs.296585; nucleolar protein (KKE/D repeat; colon, test, blad; CTL+s.m.
436278; BE395290; Hs.5097; synaplogyrin 2; pros; mAb
436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
60 436293; A1601188; Hs.306201; ESTs; blad; diag
436302; A1358841; Hs.99330; hypothetical protein FLJ23588; lung; diag
436315; BE390513; Hs.27935; hypothetical protein MGC4837; mela; diag
436396; A1683487; Hs.152213; wingless-type MMTV Integration; lung, headnk, pros, panc; diag
436420; AA443966; Hs.31595; ESTs; angio; mAb
65 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
436511; AA721252; Hs.291502; ESTs; lung; diag
436563; AW407167; Hs.181125; immunoglobulin lambda locus; lung; diag
436569; BE439539; Hs.301861; glutathione S-transferase M2 f; blad; s.m.
436614; AW104388; Hs.149091; ESTs; mela; CTL+s.m.
70 436700; A1693890; Hs.301406; hypothetical protein PP3501; mela; mAb
436729; BE621807; Hs.351318; transmembrane 4 superfamily mc; panc, colon, stom, ovar, lung, blad; mAb
436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag
436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
436839; AA767346; Hs.372277; ESTs; lung; diag
75 436856; A1683355; Hs.127310; ESTs; mela; diag
436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
437052; AA851697; Hs.120591; ESTs; pros; diag
437098; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag
80 437100; A1761073; Hs.14535; Homo sapiens cDNA: FLJ22314 f; panc, renal; diag
437119; A1379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
437145; AF007216; Hs.5462; solute carrier family 4, sodiu; panc, pros, stom; mAb
437156; A1916600; Hs.121194; Homo sapiens cDNA: FLJ21568 f; stom, renal, colon; diag
437181; A1306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

- 437204; AL110216; Hs.355861; ESTs, Weakly similar to I55214; lung; CTL+s.m.
 437212; AI765021; Hs.210775; ESTs; renal, uter, ovar; diag
 437224; AL117628; Hs.97808; ESTs; test; diag
 437259; AI377755; Hs.120695; ESTs; lung; diag
 437267; AW511443; Hs.258110; ESTs; BPH; diag
 437289; AA334384; Hs.149420; ESTs; angio; diag
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
 437381; NM_003684; Hs.5591; MAP kinase-interacting serine; glio; CTL+s.m.
 437390; AI125859; Hs.112607; ESTs; lung; diag
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
 437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag
 437437; AA226868; Hs.351823; hypothetical protein DKFZp762L; test; CTL+s.m.
 437478; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.
 437553; AI829936; Hs.130497; ESTs, Weakly similar to MAT8_H; blad; mAb
 437571; AA760894; Hs.125350; ESTs; pros; diag
 437623; D63860; Hs.5718; chromosome condensation-relate; test; diag
 437740; AA810265; Hs.122915; ESTs; mel; diag
 437802; AI475995; Hs.122910; ESTs; panc; diag
 437862; AW978107; Hs.5894; Homo sapiens mRNA; cDNA DKFZp5; mel; CTL+s.m.
 437908; AI082424; Hs.351043; ESTs; test; diag
 437915; AI837893; Hs.202312; Homo sapiens clone N11 Ntera2D; lung, headnk, ovar, blad, uter; diag
 437931; AI249468; Hs.124434; ESTs; blad; diag
 437936; AW938591; Hs.5840; mucin 13, epithelial transmembr; colon, stom, uter, panc; mAb+s.m.
 437938; AI950087; Hs.389628; gbwcq05c02.x1 NCL_CGAP_Kid12 H; renal, ovar, uter, cerv, blad; diag
 437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 437980; AI689586; Hs.369312; ESTs; uter, ovar; diag
 438167; R28363; Hs.24288; chemokine binding protein 2 (C; ovar, breast, uter; mAb
 438199; AW016531; Hs.122147; hypothetical protein FLJ13189; breast; diag
 438209; AL120658; Hs.6111; aryl-hydrocarbon receptor nuci; mel; mAb+s.m.
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag
 438274; AI918900; Hs.55080; ESTs; headnk; diag
 438403; AA806607; Hs.232206; ESTs; lung; mAb
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 438450; AI050866; Hs.65853; nodal, mouse, homolog; test; diag
 438456; AA913381; Hs.279753; ESTs; test; diag
 438552; AJ245820; Hs.6314; type I transmembrane receptor; pros, ovar; diag
 438670; AI275803; Hs.123426; ESTs; fibro; CTL+s.m.
 438702; AI879064; Hs.7184; ESTs; lung; diag
 438707; L08239; Hs.5326; amino acid system N transporter; ovar; mAb
 438746; AI865815; Hs.184727; Human melanoma-associated anti; panc, blad, mel, ovar; mAb+CTL
 438817; AI023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
 438859; AI559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag
 438866; U44386; Hs.6441; fasus inhibitor of metallopro; mel; diag
 438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fl; fibro; diag
 438898; AI819853; Hs.106243; ESTs; lung; diag
 438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, mel; diag
 438929; AW195515; Hs.253177; ESTs; renal; diag
 438958; W00847; Hs.135058; Human DNA sequence from clone; lung; diag
 438966; AW979074; ; gb:EST391184 MAGE resequences; ; renal; diag
 438983; AF065884; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.
 438993; AA828995; gb:cd77b08.s1 NCL_CGAP_Ov2 Hom; ovar; mAb+s.m.
 439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag
 439092; AA830149; ; gb:oc4408.s1 NCL_CGAP_GCB1 Hb; pros; diag
 439176; AA446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
 439180; AI393742; Hs.159067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mel; mAb
 439221; AA737108; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 439237; AW408168; Hs.318893; ESTs, Weakly similar to A47582; mel, fibro; diag
 439238; AI031540; Hs.235331; ESTs; blad; diag
 439285; AL133916; Hs.47880; hypothetical protein FLJ20083; lung, breast; diag
 439310; AF086120; Hs.102793; ESTs; mel; diag
 439318; AW837048; Hs.6527; G protein-coupled receptor 58; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mel; mAb+s.m.
 439336; AA742697; Hs.62492; NM_052863; Homo sapiens secreto; fibro, uter; diag
 439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
 439382; BE247684; Hs.103070; ESTs; angio; diag
 439394; AA149250; Hs.56105; ESTs; lung; diag
 439410; AA632012; Hs.188748; ESTs; angio; diag
 439453; BE264974; Hs.6586; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.
 439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; mel, esoph; diag
 439659; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mel, colon; mAb
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog; ovar, uter; mAb
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag
 439702; AW085525; Hs.55964; ESTs; mel; diag
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung, headnk; diag
 439735; AI635386; Hs.142846; hypothetical protein; pros; diag
 439737; AI751438; Hs.41271; Homo sapiens mRNA full length; panc; diag
 439750; AL359053; Hs.57684; Homo sapiens mRNA full length; panc, fibro, breast; diag
 439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb
 439765; AL359055; Hs.67709; Homo sapiens mRNA full length; colon, stom, panc, leuk, lung; diag
 439778; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 439780; AL109688; ; gb:Homo sapiens mRNA full leng; blad, esoph; diag
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length; ovar, uter, cerv, breast, pros; diag
 439884; AI720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
 439867; AA847510; Hs.161292; ESTs; panc; diag

- 439920; H05430; Hs.288433; neurotrophic panc; mAb+diag
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag
 439963; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 440042; A1073387; Hs.133998; ESTs; ovar; CTL+s.m.
 440086; NM_005402; Hs.6906; v-rat simian leukemia viral on; angio; diag
 440099; AL080058; Hs.6909; DKFZP564G202 protein; panc; diag
 440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag
 440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.
 440151; AA868167; ; gb:ak38a07.s1 Scarsa_testis_NH; sarc; diag
 440207; A1371978; Hs.128326; ESTs; test; diag
 440209; H05049; Hs.247837; neuraxin 3; fibro; diag
 440210; AW674562; Hs.122128; ESTs; glio; diag
 440225; BE295762; Hs.159; tumor necrosis factor receptor; glio; mAb
 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
 440260; A1972867; Hs.7130; copine IV; pros; diag
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fi; lung, fibro; diag
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
 440311; A1733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag
 440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
 440333; A1378424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fi; breast; diag
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_H; fibro; diag
 440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mela; diag
 440484; BE328156; Hs.150356; ESTs; panc; diag
 440528; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 fi; pros; diag
 440659; AF134160; Hs.7327; claudin 1; lung; mAb
 440704; M69241; Hs.162; insulin-like growth factor bin; lung, glio, ovar; diag
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag
 440801; AA906366; Hs.370038; ESTs; pros; diag
 440819; A1809444; Hs.202108; ESTs; pros; diag
 440901; AA909358; Hs.128812; ESTs; ovar; pros; diag
 440943; AW082288; Hs.146161; hypothetical protein MGC2408; lung; diag
 440983; M20681; Hs.7594; solute carrier family 2 (faci); test; mAb
 441020; W79283; Hs.35962; ESTs; lung, panc; diag
 441031; A1110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fi; panc, ovar, stom, uter, lung; diag
 441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
 441321; H17182; Hs.7771; B-cell associated protein; test; diag
 441345; AW088579; Hs.7780; Homo sapiens mRNA: cDNA DKFZp5; pros; diag
 441350; AB202690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL
 441377; BE218238; Hs.202656; ESTs; uter, endo, lung; diag
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
 441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag
 441457; AW996851; Hs.43838; ESTs; angio; diag
 441495; AW294603; Hs.127038; ESTs; blad; diag
 441525; AW241867; Hs.127728; ESTs; lung; diag
 441553; AA281219; Hs.121298; ESTs; lung, test, ovar; CTL+s.m.
 441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
 441790; AW294909; Hs.132208; ESTs; lung; diag
 441801; AW242799; Hs.86366; ESTs; blad; diag
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
 441859; AW194364; Hs.380444; interleukin-4 induced gene-1 p; ovar, mela, fibro; mAb
 441878; A1801889; Hs.127982; ESTs; test; diag
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.
 442082; R41823; Hs.7413; calyculin-2; breast, pros, ovar; diag
 442104; L20571; Hs.188; phosphodiesterase 4B, cAMP-spe; angio; CTL+s.m.
 442108; AW452649; Hs.343259; ESTs; lung; diag
 442242; AW647908; Hs.90424; Homo sapiens cDNA: FLJ23286 fi; BPH; diag
 442323; AW016668; Hs.29190; ESTs; breast; diag
 442333; A1850877; Hs.129302; ESTs; test; diag
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mela; CTL+s.m.
 442438; AA985998; Hs.370007; gb:os26b03.s1 NCL_GAP_Kid5 Ho; uter, ovar, renal; diag
 442441; A1820662; Hs.129598; ESTs; breast; diag
 442503; AF147078; Hs.375031; p53-responsive gene 5; mela; diag
 442506; BE556411; Hs.41726; ESTs; angio; diag
 442573; H93366; Hs.7567; branched chain aminotransferas; ovar, panc, angio, test; s.m.
 442577; AA282998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag
 442580; A1733882; Hs.130239; ESTs; breast; diag
 442609; AL020896; Hs.8518; selenoprotein N; mela; diag
 442613; A1004002; Hs.130522; Kv channel-interacting protein; glio; diag
 442622; NM_000435; Hs.8546; Nckh (Drosophila) homolog 3; ovar; mAb
 442711; AF161073; Hs.8645; hypothetical protein; angio, mela, sarc; diag
 442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mela; s.m.
 442757; A1739528; Hs.28345; ESTs; mela; diag
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 442821; BE391829; Hs.8752; transmembrane protein 4; ovar; diag
 442832; AW203560; Hs.253569; ESTs; pros, fibro; diag
 442895; R37725; Hs.283093; ESTs; panc; diag
 442994; A1028718; Hs.16954; ESTs; blad, fibro; diag
 443054; A1745185; Hs.84520; yes-associated protein 85 kDa; blad; diag
 443162; T49851; Hs.9028; DKFZP434G032 protein; blad, lung; CTL+s.m.
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

- 443184; A1838728; Hs.135159; ESTs; sarc; diag
 443211; A1128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag
 443216; W80487; Hs.324521; hypothetical protein DC50; test; diag
 443257; A334040; Hs.11614; HSPC065 protein; fibro; CTL+s.m.
 443400; R28424; Hs.260648; ESTs; lung; diag
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.
 443537; D13305; Hs.203; cholecystikinin B receptor; test; mAb
 443648; A1085377; Hs.143610; ESTs; lung, headnk; diag
 443709; A1082692; Hs.134682; ESTs; fibro; diag
 443715; A1583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
 443785; AW449552; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
 443883; AA114212; Hs.9930; serine (or cysteine) proteinase; sarc; s.m.
 443885; H91806; Hs.15284; ESTs; mela; diag
 443892; A1889572; Hs.246675; ESTs; lung; diag
 443950; NM_001425; Hs.9999; epithelial membrane protein 3; mela; mAb
 443966; AA287702; Hs.10031; KIAA0955 protein; angio; diag
 443983; H04482; Hs.163724; ESTs; mela; mAb
 443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
 444009; A1380792; Hs.135104; ESTs; angio; diag
 444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like; test; CTL+s.m.
 444163; A1126098; ; FGENESH predicted RNaseH domain; blad; s.m.
 444301; AK000136; Hs.10780; espinin (LRR class 1); panc; diag
 444325; AW152618; Hs.16757; ESTs; esoph; diag
 444330; A1597655; Hs.49265; ESTs; angio; diag
 444342; NM_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
 444378; R41339; Hs.47860; neurotrophic tyrosine kinase; lung, glio; mAb+s.m.
 444409; A1792140; Hs.49265; ESTs; angio; diag
 444444; A1149332; Hs.14855; ESTs; blad; diag
 444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon; mAb
 444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (N); blad; s.m.
 444484; AK0002126; Hs.11250; hypothetical protein FLJ11264; pros; diag
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
 444649; AW207523; Hs.371001; ESTs; blad; diag
 444670; H63873; Hs.332938; hypothetical protein MGC5370; sarc; diag
 444764; T83911; Hs.11891; transmembrane 4 superfamily me; panc, omuc, stom, lung, colon; mAb+s.m.
 444809; BE207568; Hs.208219; oculospantin; mela; mAb
 444823; BE262989; Hs.12045; putative protein; test; diag
 444853; AW384082; Hs.104678; serine (or cysteine) proteinase; mela; s.m.
 444895; A674363; Hs.22891; solute carrier family 7 (cat); ovar; mAb+s.m.
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
 445019; A1205540; Hs.281295; ESTs; headnk, lung, colon; diag
 445070; NM_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb
 445076; A1206888; Hs.154131; ESTs; test; diag
 445084; H38914; Hs.250948; hypothetical protein FLJ14761; sarc; mAb
 445093; A1207197; Hs.166905; ESTs; test; diag
 445109; AF039916; Hs.12330; adenosine triphosphate d; pros; s.m.
 445118; AF035121; Hs.12337; kinase insert domain receptor; angio; mAb
 445160; A1299144; Hs.101937; sine oculis homeobox (Drosophila); sarc; CTL+s.m.
 445182; AW189787; Hs.361778; ESTs; blad; diag
 445247; AW274290; Hs.153997; ESTs; mela; diag
 445279; R41900; Hs.22245; ESTs; angio; diag
 445383; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
 445413; AA151342; Hs.12677; CG-147 protein; pros, colon, uter, ovar, panc; diag
 445418; AW193977; Hs.127179; cryptic gene; panc; diag
 445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros; diag
 445443; AV653838; Hs.295131; ESTs; lung; diag
 445554; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
 445584; AK001696; Hs.13109; Ran binding protein 11; angio; diag
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
 445784; A1253155; Hs.146065; ESTs; mela; CTL+s.m.
 445885; A1734009; Hs.127699; KIAA1603 protein; pros, fibro; diag
 445900; AF070526; Hs.125035; Homo sapiens clone 24787 mRNA; renal, leuk; mAb
 445911; A1985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag
 445982; BE410233; Hs.13501; pascadillo (zebrafish) homolog; mela; diag
 446057; A420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb
 446082; A1274139; Hs.156452; ESTs; blad; diag
 446098; AW072216; Hs.208470; ESTs; angio; diag
 446100; AW987109; Hs.13804; hypothetical protein dJ462023; pros; diag
 446102; AW168067; Hs.317694; ESTs; lung; diag
 446113; AW987553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
 446269; AW253155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
 446291; BE397753; Hs.14623; Interferon, gamma-inducible p; mela; diag
 446292; AF081497; Hs.279882; Rn type C glycoprotein; lung, cerv; mAb
 446293; A1420213; Hs.149722; LIM domain transcription facto; ovar, test; diag
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase; pros; s.m.
 446332; AKJ01635; Hs.14636; hypothetical protein FLJ10773; breast; diag
 446342; BE298665; Hs.14846; solute carrier family 7 (cat); uter, colon, pros, mela; mAb
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALJ4_1; fibro; diag
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag
 446608; N75217; Hs.175622; ESTs; uter, fibro; diag
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
 446644; NM_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb
 446673; NM_016361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag
 446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
 5 446733; AA863360; Hs.28040; ESTs, Weakly similar to fatty; breast; s.m.
 446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.
 446791; A1532276; Hs.185922; ESTs; test; diag
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
 10 446856; A1814373; Hs.164175; ESTs; lung; diag
 446868; AV660737; Hs.348297; ESTs; panc; diag
 446872; X97058; Hs.16362; pyridinergic receptor P2Y, G; lung; mAb
 446932; AA961459; Hs.125644; ESTs; fibro; diag
 446967; A1699829; Hs.156781; ESTs; fibro; diag
 15 446979; A1654443; Hs.197683; ESTs; test; diag
 446984; AB020722; Hs.15714; Rho guanine exchange factor (G; angio; CTL+s.m.
 446989; AK001898; Hs.15740; hypothetical protein FLJ11036; lung, headnk; diag
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
 446999; AA151520; Hs.351418; hypothetical protein MGC4485; headnk; diag
 20 447004; AW296956; Hs.157539; FGENESH predicted secreted pro; glio; diag
 447076; AW885727; Hs.5914; ESTs; lung; diag
 447126; AW150632; Hs.170307; Rat guanine nucleotide exchang; angio; diag
 447164; AF026941; Hs.17518; vifilin; similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
 447178; AW594641; Hs.192417; ESTs; mela; diag
 25 447188; H65423; Hs.17634; hypothetical protein DKFZp434E; test; diag
 447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.
 447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
 447334; AA516032; Hs.91109; ESTs; blad; diag
 447343; AA256841; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
 30 447350; A375572; Hs.172634; v-erb-b avian erythroblastic l; breast, ovar, uter; diag
 447377; X77343; Hs.334334; transcription factor AP-2 alphi; breast, lung, mela; CTL+s.m.
 447395; A1418412; Hs.184793; Homo sapiens cDNA: FLJ21880 f; panc; diag
 447437; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar; mAb+s.m.
 35 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
 447534; AW953935; Hs.288655; ESTs; lung, test; diag
 447578; AA912347; Hs.136685; ESTs, Weakly similar to JC5314; ovar; s.m.
 447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag
 40 447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.
 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
 447749; T53280; Hs.8297; ESTs; renal; diag
 447761; AF061573; Hs.19492; protocadherin 8; EWS, glio; mAb
 447768; X86400; Hs.19520; FXVD domain-containing ion tra; renal; mAb
 447818; W79940; Hs.355279; Homo sapiens clone 24570 mRNA; renal; diag
 447835; AW591623; Hs.164129; ESTs, Weakly similar to J38022; renal, ovar, uter; diag
 447881; BE620888; Hs.355279; GCN1 (general control of amino; renal; diag
 447937; AL109716; Hs.20034; Homo sapiens mRNA full length; mela; mAb
 447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 50 448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom; lung; mAb
 448045; AJ297436; Hs.20168; prostate stem cell antigen; blad, panc, pros; mAb
 448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
 448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb
 448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb
 55 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase; test; CTL+s.m.
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
 448204; AJ475124; Hs.170551; ESTs; sarc; diag
 448231; AJ701916; Hs.202509; ESTs; angio; diag
 448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
 448262; AW890830; Hs.186273; ESTs; blad; diag
 60 448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag
 448278; W07369; Hs.11782; ESTs; lung; diag
 448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 f; pros; diag
 448321; NM_005083; Hs.20912; adenomatous polyposis coli lfc; glio; CTL+s.m.
 448357; N20169; Hs.108823; RAB38, member RAS oncogene fam; lung, mela; diag
 65 448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
 448437; AW470125; Hs.220529; gbxxw60c04.x1 NCL_CGAP_Pan1 Ho; panc, colon; diag
 448499; BE613280; Hs.77550; p53-regulated DDA3; glio; diag
 448509; BE382657; Hs.21486; signal transducer and activator; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.
 448588; AJ970278; Hs.156905; KIAA1676; test; CTL+s.m.
 70 448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb
 448654; AJ879317; Hs.334691; splicing factor 3a, subunit 1; mela; CTL+s.m.
 448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag
 448692; AW013907; Hs.187531; methylcrotonoyl-Coenzyme A car; pros; s.m.
 448706; AW281095; Hs.21814; Interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
 75 448719; AA033627; Hs.21858; trinucleotide repeat contain; mela, sarc; CTL+diag
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate; test; diag
 448811; A1590371; Hs.199460; ESTs; esoph, panc; mAb
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.
 448966; AW372914; Hs.86149; phosphoinositol 3-phosphate-bi; mela; CTL+s.m.
 80 448981; AJ968719; Hs.195387; ESTs; test; diag
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
 448993; AJ471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
 448999; AF178274; Hs.22791; transmembrane protein with EGF; pros, glio; mAb

- 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class); lung, headnk; s.m.
 449019; A194095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
 449027; AJ271216; Hs.22880; dipeptidylpeptidase II; blad, colon, ovar; s.m.
 449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
 449078; AK001255; Hs.22975; KIAA1576 protein; mel; diag
 449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
 449108; AW270992; Hs.120943; ESTs, Weakly similar to ALU7_H; sarc; diag
 449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
 449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag
 449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag
 449230; BE613348; Hs.355392; melanoma cell adhesion molecule; lung, cerv, headnk, blad, ovar, colon; mAb
 449317; AW293413; Hs.132906; 19A24 protein; mel; mAb
 449318; AW236021; Hs.78631; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.
 449322; A1638616; Hs.196566; ESTs; test; diag
 449338; H73444; Hs.394; adrenomedullin; renal; diag
 449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 f1; angio; mAb
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1; test; diag
 449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag
 449467; AW205006; Hs.197042; ESTs; lung; diag
 449494; AW237014; Hs.315389; aquaporin 4; fibro; diag
 449568; A1656634; Hs.195389; ESTs; test; diag
 449592; A1655494; Hs.195718; ESTs; panc; diag
 449618; A1074549; Hs.15978; KIAA1272 protein; angio; diag
 449625; NM_014253; Hs.349094; odz (odd Ozten-m, Drosophila); pros; diag
 449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb
 449680; A1033821; Hs.12160; ESTs; renal; diag
 449681; AW265634; Hs.133100; ESTs; glo, esoph, lung, blad; diag
 449676; H08360; Hs.135056; Human DNA sequence from clone; lung; diag
 450096; A1682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 450149; AW989781; Hs.132863; Zinc family member 2 (odd-paire; sarc; CTL+s.m.
 450152; A1136635; Hs.22968; Intron of VEGFR; renal; diag
 450377; AB033091; Hs.355825; KIAA1265 protein; ovar, colon; diag
 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 f1; pros; diag
 450400; A1694722; Hs.279744; ESTs; panc; diag
 450431; AW136797; Hs.266041; ESTs; test; diag
 450451; AW591528; Hs.202072; ESTs; uter, endo; diag
 450506; NM_004460; Hs.418; fibroblast activation protein.; panc, esoph; diag
 450534; A1570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.
 450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
 450635; AW403954; Hs.25237; mesenchymal stem cell protein; blad; mAb
 450642; R39773; Hs.7130; copine IV; pros; diag
 450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
 450663; H43540; Hs.25292; ribonuclease H1, large subunit; mel; s.m.
 450676; A1147155; Hs.279727; ESTs; sarc; diag
 450684; AA872605; Hs.25333; Interleukin 1 receptor, type I; blad, lung, headnk; mAb
 450690; AA296696; Hs.333418; FXD domain-containing lon tra; mel; diag
 450693; AW450461; Hs.203965; ESTs; pros, uter; diag
 450719; A1096837; Hs.21349; ESTs, Weakly similar to REBB_H; test; diag
 450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 450785; AA852713; Hs.108985; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 450832; AW970602; Hs.105421; ESTs; lung; diag
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glo; diag
 451035; AU076785; Hs.430; plastin 1 (l isoform); panc; diag
 451050; AW937420; Hs.351869; ESTs; mel; diag
 451089; R52795; Hs.25954; interleukin 13 receptor, alpha; glo, fibro, mel; mAb
 451108; BE382701; Hs.25960; N-MYC oncogene; test, ovar; CTL+s.m.
 451110; A1955040; Hs.265396; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
 451181; A1796330; Hs.207461; ESTs; panc; diag
 451253; H48298; Hs.26126; claudin 10; lung, ovar, panc; mAb
 451291; R39288; Hs.6702; ESTs; lung; diag
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag
 451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1); lung; s.m.
 451348; NM_006330; Hs.26312; glioma amplified on chromosome; ovar; mAb
 451386; AB029008; Hs.26334; specific paraplegia 4 (autosome; lung; diag
 451398; A1793124; Hs.144478; ESTs; breast, ovar; diag
 451411; AA017492; Hs.135656; EST; pros; diag
 451497; H63294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
 451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag
 451592; A1805416; Hs.213897; ESTs; lung, headnk; diag
 451635; AA018899; Hs.127178; cryptic gene; panc; diag
 451663; A1872360; Hs.209283; ESTs; pros; diag
 451720; AW970985; Hs.290853; ESTs; pros; diag
 451743; AW074288; Hs.336428; ESTs; lung; diag
 451820; AW058357; Hs.199248; ESTs; panc; mAb
 451844; T61430; ; gbxyc06a03.s1 Stratagene lung; blad; diag
 451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb
 451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/His) b; test; CTL+s.m.
 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
 452208; AA024792; Hs.31895; hypothetical protein MGC4083; renal; diag
 452240; A1591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
 452243; AL355715; Hs.28555; programmed cell death 9 (PCD9; breast; diag
 452244; N33530; Hs.176674; ESTs; mel; diag

- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, 8; test; CTL+s.m.
 452295; BE379936; Hs.28866; programmed cell death 10; lung; diag
 452298; AI039243; Hs.278586; ESTs; angio; diag
 452304; AA026386; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
 452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb
 452367; U71207; Hs.29279; eyes absent (Drosophila) homolog; lung, pros, ovar, uter; CTL+s.m.
 452416; AA026116; Hs.114777; ESTs; fibro; diag
 452461; N78223; Hs.108108; transcription factor; blad, lung, headnk, ovar, glio, stom, colon, cerv; CTL+s.m.
 452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag
 452594; AU076406; Hs.29981; solute carrier family 26 (sulf; ovar; mAb
 452613; AA481599; Hs.23459; ESTs; lung; diag
 452679; Z42367; Hs.83883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
 452705; H49805; Hs.246005; ESTs; panc; diag
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag
 452721; AJ269629; Hs.301871; solute carrier family 37 (glyc; pros; mAb
 452732; BE300078; Hs.80448; Homo sapiens, clone IMAGE:3535; blad; diag
 452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; mela; diag
 452792; AB037765; Hs.30662; KIAA1344 protein; pros, uter, breast; diag
 452795; AW392555; Hs.18978; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
 452833; BE559681; Hs.30736; KIAA0124 protein; lung, mela; CTL+s.m.
 452865; AJ924046; Hs.119567; ESTs, Weakly similar to A47682; lung; diag
 452899; M95739; Hs.30956; nescent helix loop helix 1; sarc; CTL+s.m.
 452924; AW580839; Hs.97199; complement component C1q recep; angio; diag
 452933; AW391423; Hs.28855; Homo sapiens cDNA: FLJ22425 f; angio; CTL+s.m.
 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.
 453006; AI862575; Hs.303171; ESTs; pros; diag
 453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.
 453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag
 453096; AW294631; Hs.351270; ESTs; pros; diag
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog; lung, headnk, colon; mAb
 453107; NM_016113; Hs.279746; vanilloid receptor-like protel; mela; mAb
 453134; AA032211; Hs.118493; ESTs; blad; diag
 453142; AA033646; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
 453160; AJ263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag
 453210; AL133161; Hs.32360; hypothetical protein FLJ10867; lung; CTL+s.m.
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
 453256; AI565687; Hs.32556; KIAA0379 protein; mela; diag
 453310; X70897; Hs.553; solute carrier family 8 (neuro; fibro; mAb
 453321; AI984381; Hs.232521; ESTs; blad; diag
 453323; AF034102; Hs.32951; solute carrier family 29 (nucl; ovar; CTL+s.m.
 453331; AI240865; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
 453344; BE349075; Hs.44571; ESTs; mela; diag
 453346; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
 453365; AA036211; Hs.17404; SOX7 SRY (sex determining reg; angio, blad; CTL+s.m.
 453370; AI470523; Hs.139396; ATP-binding cassette, sub-fam; pros; mAb
 453389; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.
 453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glio, sarc; CTL+s.m.
 453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag
 453464; AI884911; Hs.32988; receptor (calcitonin) activity; pros; mAb
 453633; AA357001; Hs.34045; hypothetical protein FLJ20784; lung, esoph, test; diag
 453637; NM_002589; Hs.34073; BH-proteocadherin (brain-heart); headnk; mAb
 453642; AI370536; Hs.34074; dipeptidylpeptidase VI; glio; mAb
 453779; N35187; Hs.43388; 28kD interferon responsive pro; mela; diag
 453789; AA628517; Hs.118502; ESTs; angio; diag
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glio, lung, uter, headnk, cerv, panc, pros, sarc; mAb
 453863; AI638816; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
 453884; AA355825; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag
 453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; mela; diag
 453922; AF063306; Hs.36708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.
 453935; AI633770; Hs.42572; ESTs; panc; diag
 453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
 453964; AI961486; Hs.249196; ESTs; lung; diag
 453966; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 453985; N44545; Hs.251865; ESTs; test; diag
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 fam; lung, headnk; s.m.
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
 454066; X00356; Hs.37058; calcitonin/calcitonin-related; lung; diag
 454071; AI041793; Hs.42502; ESTs; breast; diag
 454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); test; diag
 454098; W27953; Hs.217493; Plakophilin; lung; diag
 454117; BE410100; Hs.40388; adaptor-related protein complex; mela; CTL+s.m.
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fam; glio; mAb
 454429; BE273437; Hs.301406; hypothetical protein PP3501; mela; mAb
 454435; AW819152; Hs.154320; DKFZP580C1645 protein; lung; diag
 454478; AW805749; Hs.372783; superoxide dismutase 2, mito; mela; s.m.
 455601; AI388680; Hs.818; SRY (sex determining region Y); lung, cerv, esoph; s.m.
 456034; AW450979; ; gb-U1-H-B3-ata-a-12-Q-U1.s1 N; blad, fibro; diag
 456052; AI866286; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag
 456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.
 456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL
 456553; AA721325; Hs.189058; ESTs, Highly similar to Smila; panc; diag
 456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.
 456736; AW248217; Hs.1619; achaete-scute complex (Drosoph); lung; diag
 456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio; lung; mAb
 456847; AJ360456; Hs.86088; ESTs; test; diag
 456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.
 456977; AK000252; Hs.168758; hypothetical protein FLJ20245; angio; diag
 457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.
 457211; AW972565; Hs.32399; ESTs, Weakly similar to S61797; meta; pros; CTL+s.m.
 457292; AI921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb
 457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.
 457411; AW085861; Hs.130093; iroquois-class homeobox protein; breast, fibro; diag
 457465; AW301344; Hs.122908; DNA replication factor; test; meta; diag
 457498; AJ732230; Hs.191737; ESTs; pros; diag
 457561; AA331517; Hs.286055; chimerin (chimerin) 2; glio; mAb
 457590; AJ612809; Hs.5378; hypothetical protein MGC10724; ovar; diag
 457869; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 458092; W67353; Hs.350558; KIAA0251 protein; lung; diag
 458124; AW005548; Hs.124590; ESTs; fibro; diag
 458435; AJ418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag
 458471; AV848609; Hs.184240; ESTs; renal, panc, hepC; diag
 458933; AJ638429; Hs.24763; RAN binding protein 1; lung, test; diag
 459373; BE408286; Hs.301408; hypothetical protein PP3501; meta; mAb
 459578; AW612538; Hs.304491; EST; meta; diag
 459702; AJ204995; g; gbxan03c03.x1 Stratagene schiz; blad, fibro; diag
 459706; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075778 AA075221 AA076395 AA650486 AA083500
108282	108971_1	AA065143 AA065142
113230	2327174_1	AI820546 AI821336 T61430
118417	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW205802 AI583718 AF080231 AF080234 AF080233 AL535584
		AI618326 AF080230 S45404 AI970576 AA463392 AW655466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614851
		N29586 N25595 H65001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N60448 BE219539 BE671665 AI624817 BE466811
		AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF082180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833
		AA207155 BI004756 AA206262 AI365204 H77608 AW590511
		AA404418 AI217248
		AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
		AF147347 T55603 T55426
		C16391 C16413
		AI629520 AI791832 AI791823 AA229315 AA228414 AA229211
		AA410943 BF386582 AA334202 AA332682 BF371899 AW948853
		AL044891 AI908240 AA393080 AW748403 BE065341 BF330573
		M18728
		AA075419 AA082953 AA080912 AA052835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892
		AA076318 AA076594 AA078900 AA134801 AA063293 AA083403 AW974305
		AA070050 AA070823 AA063403
		BI030997 AA921674 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722
		BI007625 BI027884 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762
		BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
		BE088101 T05990 AW872477
		BE168258 BE168190 T64882
		AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
		AA210987 D57294 AA214584 AA207006 D56572
		AA401424 AA400100 AA663848
		AA833717 BF061897 AW628327 AA641788 AA400495
		AW973362 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF058601 AI861162 AI341422 AI206248 AI206165
		AA548736 AA768578 AI639081 AW025957 AA736837 N79576 AW594357 AA480892
		AW874271 AA592975 AA447312 AA884768
		AA527941 AA636266 AI810608 AI620180
		BG207209 BE166299 AI204896 BG196355 AW969808 AA528756 AW440776 BI044354
		BG036675 BF772005 BF771866 BG980386 BG950381 NM_005712 AF110315 BE074534 BE182776 BE168000 BE157999 BE714315 AW818104
		AW847519 AA099426 AW817881 AW856386 BG861122 AA224498 AA308542 AW821833 BF902156 AI732411 BG776834 BG283841 BE748279
		BE748870 BG319540 BE748864 BF738224 BG886155 AK057283 BI861466 AA663341 AA457591 BG849294 AW392886 AA071122 AA227849
		AA584918 BG559570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF789107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW981687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055582
		BG166382 AW181086 N42363 BE935013 BE934998 BG291451 AV700520 BG152773 AI224956 AI079635 AW054706 AA843979 AI744193 F04050
		T23457 F04044 AA723859 AA977643 AA283764 AI123609 N21561 BF055052 BE856861 AI804220 AA843394 AI472045 AI740490 AA578830
		H05495 AI283334 AA809495 AI122773 AW162643 AW161798 BF940077 AI808825 AJ360886 AI123189 R40236 R20726 AW975899 BE764052
		N31709 N31708 AI031947 AW194138
		AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
		AA055656 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298

AA223287 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
 BF684337
 434596 14701_1 AF147374 T59538 T59589 T59598 T59542
 434609 14739_1 AF147390 R76593 R76594
 438966 1242593_1 AW979074 AA834841 AA828650
 438993 2580163_1 AIS26361 AA834879 AA826995
 439092 919640_1 AW978407 AA830149 M85983 AW503637 BF352096
 439780 49082_1 AL109688 R23665 R26578
 440151 1879911_1 AA868167 F21558 F31418 F35624
 444163 682245_1 BG403189 AI148521 AI184746 AI126098 RD5933 BI057330
 451844 2327174_1 AI820546 AI821336 T61430
 456034 685586_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
 459702 539529_1 BG207209 BE166299 AI204996 BG199355 AW968908 AA528756 AW440776 BI044354

15 TABLE 3C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
325372	5866820	Minus	1117061-1117304
325544	6682452	Plus	171228-171286
327036	6531965	Plus	319951-320040
327075	6531965	Plus	4041318-4041431
327414	5867750	Plus	102481-102586
328700	5868264	Plus	764089-764203
330211	6013582	Plus	59158-69215
332798	Dunham, I. et al.	Minus	232147-231974
333769	Dunham, I. et al.	Plus	7696625-7696707
333904	Dunham, I. et al.	Minus	8217374-8217261
334223	Dunham, I. et al.	Minus	12734365-12734269
334447	Dunham, I. et al.	Plus	14308764-14308824
335115	Dunham, I. et al.	Minus	21388250-21388146
335809	Dunham, I. et al.	Plus	26310772-26310909
335824	Dunham, I. et al.	Plus	26376860-26376942
335825	Dunham, I. et al.	Plus	26378175-26378268
335936	Dunham, I. et al.	Minus	27360474-27360400
336034	Dunham, I. et al.	Plus	29014404-29014590
336152	Dunham, I. et al.	Minus	30155053-30155870
336836	Dunham, I. et al.	Plus	988418-988185
338008	Dunham, I. et al.	Plus	7697068-7697236
338033	Dunham, I. et al.	Plus	8092128-8092271
338158	Dunham, I. et al.	Minus	11794465-11794343
338265	Dunham, I. et al.	Minus	15242294-15242231
400494	9714719	Plus	169845-170272
400517	9796686	Minus	49998-50346
400651	8117978	Minus	81488-81646
400665	8118496	Plus	16879-17023
400773	8131629	Minus	44116-44238,48208-48321
400844	9188905	Plus	24746-24872,25035-25204
400846	9188605	Plus	39310-39474
400881	2842777	Minus	91446-91603,92123-92265
401093	8516137	Minus	22335-23166
401234	9929642	Plus	120173-120337
401424	8176894	Plus	24223-24428
401466	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
401704	3097841	Plus	24712-25374
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
401747	9789672	Minus	118596-118816,119119-119244,119809-11978
401760	9929699	Plus	83128-83260,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401785	7249190	Minus	165776-165986,166189-166314,166408-16656
401797	6730720	Plus	6973-7118
401994	4153958	Minus	42904-43124,43211-43336,44607-44763,4519
402145	8018280	Plus	113088-114800
402189	8576118	Minus	84187-84744
402230	9866312	Minus	29782-29932
402239	7690131	Plus	38176-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
402265	3287673	Plus	21059-21168
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402424	9796344	Minus	64925-65073
402447	9796540	Plus	47605-47729,51096-51821,52070-52257,5330
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402550	7652009	Minus	80413-80573
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973

	402606	9909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402777	9588235	Plus	126786-126948
5	402860	9588237	Minus	76423-76560
	402888	9930692	Minus	54727-54901
	402992	7767907	Minus	42137-42515
	402994	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137095
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
15	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
20	403715	7239669	Plus	85128-85292
	403740	7630882	Plus	86504-87227
	403776	7770511	Minus	1414-1513,1624-1756
	403903	7710571	Minus	101165-102597
	404029	7671252	Plus	108716-111112
25	404049	3688074	Minus	75765-78155
	404210	5005246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404253	9367202	Minus	55675-56055
	404286	2326514	Plus	51086-51301
30	404298	9944263	Minus	73691-73723
	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404868	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68650-69563
	404998	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-15188
	405451	7622517	Minus	145849-146227
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
45	405547	1054740	Plus	124361-124520,124914-125050
	405646	4914360	Plus	741-969
	405704	4204244	Plus	138842-139061
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405932	7787812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71754-71944
55	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-8077
60	406547	7711513	Minus	172780-174368

65 Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eco-Hu03 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

70 Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. phosphatase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

75	Key:	Unique Eco probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
80	UniGene Title:	UniGene gene title
	R1:	Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Key	ExAccn	UniGeneID	Pred.Prod.Domains	UniGeneTitle	R1
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5	419551	AW582256	Hs.91011	TM=M;SS=M	anterior gradient 2 (<i>Xenopus laevis</i>)	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
	409340	BE174829	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	strafin	6.4
	417931	W95642	Hs.82961	trefoil;TM=N;SS=M	trefoil factor 3 (intestinal)	6.3
	447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of Target Exon	6.1
10	406387					6.0
	421814	L12350	Hs.108623	EGF,isp_1,vwc,TSPN,isp_3;	thrombospondin 2	5.8
	406867	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	5.8
	426104	A1204418	Hs.190080		ESTs	5.8
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
15	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (<i>Drosophila</i>) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transporter	5.5
	419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
	418344	AA216387			gbcn18b02.s1 NCLCGAP_P1 Homo sap	5.2
	407116	AA130986	Hs.271627		ESTs	5.1
20	417389	BE260984	Hs.82045	PTN_MK;TM=M;SS=Y	midline (neurite growth-promoting f	5.1
	419452	U36335	Hs.90572	Ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026892	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
	409453	AI685518	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
25	417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regula	5.0
	422087	X58968	Hs.111301	fn2,hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	Ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily contain	4.9
30	408491	AI088063	Hs.7882		ESTs	4.9
	417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
	408062	AL157486	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
	422281	M36803	Hs.346935	hemopexin;TM=N;SS=M	hemopexin	4.9
	425308	M97639	Hs.155585	ig,kningle,pkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
35	408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
	448019	AB949395	Hs.87776		ESTs, Weakly similar to T22341 hypo	4.8
	435561	AA351878	Hs.4943	MAGE,Cys_kno1,EGF,laminin	hepatocellular carcinoma associated	4.8
	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
	428455	AI472111	Hs.278694	lectin_c	CD209 antigen	4.8
40	414407	AA147026	Hs.76704		ESTs	4.8
	419390	AF011182	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
45	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
	449717	AB040935	Hs.24394	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	AB917901	Hs.208641	actin,none	ESTs	4.6
	435370	AB84074	Hs.225838	EGF,fn3,fibrinogen_C,tox	ESTs	4.6
	411761	AF733948	Hs.71936	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	AJ243706	Hs.143323	PHD,ARID,im(C),im(N),zf-C5H	putative DNAchromatin binding moti	4.6
50	426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.6
	408796	AA586292	Hs.170345	hormona_rec,zf-C4	ESTs	4.6
	407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
	422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
	447528	AB12027	Hs.76277	TB2_DP1_J_VA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
55	430168	AW568343	Hs.145582	ethand,ethand	DKFZP4341735 protein	4.4
	423225	AA952904	Hs.125389	ig,Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156642	Hs.72127	homeobox_HLH	ESTs	4.4
	452683	AB089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
	444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
60	453857	AL080236	Hs.35861	TM=Y;SS=M	Ras-induced senescence 1 (RIS1)	4.4
	413959	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
	440369	AW178150	Hs.132449		downstream of breast cancer antigen	4.3
	418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
	441384	AA447849	Hs.288650	7tm_3,none	retinoic acid induced 3	4.3
65	424464	R68537	Hs.17952	homeobox,none	ESTs	4.3
	423582	BE000631	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
	433320	D60647	Hs.250879	rm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW009888	Hs.118258		prostate cancer associated protein	4.2
70	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
	448913	AA194422	Hs.22564	rm,zf-RanBP,pkinase,GST_	myosin VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
	400486			TM=Y;SS=N	ENSP00000224716:GTP-binding protei	4.2
	442589	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
75	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to K9022 hypo	4.2
	428485	NM_006207	Hs.170040	ig;TM=N;SS=M	platelet-derived growth factor rece	4.2
	435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	tufelin 1	4.2
	446051	BE048061	Hs.37054	EphrinA_2,sem1n,dsm,z-el	ephrin-A3	4.2
80	451982	F19036	Hs.27373	NA/NA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa,integrin_A,FC-GAP;TM=	integrin, alpha 2 (CD49b, alpha 2 a	4.1
	434449	AW953484	Hs.3849	ethand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	4.1

5	423057	AW961597	Hs.130816	HLH;TM=M;SS=N	ESTs, Moderately similar to I38022	4.1
	452063	R53185	Hs.32366	ras:none	ESTs, Weakly similar to TWST_HUMAN	4.1
	450880	AF131784	Hs.25318	Peptidase_C1;TM=N;SS=M	Homo sapiens clone 25184 mRNA seque	4.1
	418283	S79895	Hs.83942		calhepsin K (pseudodysostosis)	4.1
	416351	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.184101	7tm_3:none	Homo sapiens cDNA: FLJ20869 fls, cl	4.1
	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
10	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
	448826	AI580252	Hs.255665		ESTs, Weakly similar to putative p1	4.0
	419548	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (4.0
15	421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fls, cl	4.0
	417363	AW129367	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
20	452239	AW379378	Hs.356269		protein tyrosine phosphatase, recep	4.0
	444286	AI625304	Hs.201008		ESTs	4.0
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
	451304	M92642	Hs.26208	Collagen,TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
25	441094	U33819	Hs.7647	zf-C2H2_LJM,PHD,TFIIS;TM=	MYC-associated zinc finger protein	4.0
	407788	BE514982	Hs.39991	ethand,S_100,S_100,ethand	S100 calcium-binding protein A2	4.0
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2:none	synaptotagmin 1	3.9
	433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
30	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2,ubredoxin;TM=M;S	trichorhinophalangial syndrome 1 gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serina (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
	453680	AI003166	Hs.135121	HSP70:none	ESTs, Weakly similar to I38022 hypo	3.9
35	424125	M31689	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
	437377	AL359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422562	AI962060	Hs.118397	Zn_carcOpept,F5_F8_type..C	AE-binding protein 1	3.9
	422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
40	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fls, clo	3.9
	411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Cre	3.9
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87018		hypothetical protein FLJ22938	3.8
	452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
45	421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fls, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92579	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HLH,homeobox:none	Homo sapiens cDNA FLJ12900 fls, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calysentenin-2	3.8
	423940	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	428742	AA383828	Hs.181131		ESTs	3.8
	435818	AA700553	Hs.388614	arf,ras,RecR:none	ESTs	3.8
	420005	AW271106	Hs.133294		ESTs	3.8
55	410867	X63556	Hs.760	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
	448029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
60	443933	AI091631	Hs.203845	Ion_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
	432952	AA813687	Hs.188173		Homo sapiens cDNA FLJ12187 fls, clo	3.8
	424036	AA770688	Hs.348485	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
	453328	AW970960	Hs.293821	Pep_M12B_propep,Reprolys	ESTs	3.7
	407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox:none	ESTs	3.7
	424651	AM93206	Hs.120785		ESTs	3.7
	409178	BE393948	Hs.50815	trypsin;TM=M;SS=Y	kallikrein 5	3.7
	417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
	431194	D43704	Hs.250712	Ca_channel_B,RepB_protein	calcium channel, voltage-dependent,	3.7
70	430397	AI824533	Hs.105807	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
	416969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW368377	Hs.137568	SAM,P53;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
	418840	AI821514	Hs.185831		ESTs	3.7
75	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.369982	thyroglobulin_1,IGFBP,zf-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neurostatin	3.7
	436114	AA775483	Hs.288936	ODC_AZ,Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
	416899	BE262645	Hs.80420	IL8;TM=M;SS=M	small inducible cytokine subfamily	3.7
80	422110	AI378736	Hs.121555	kazal:none	secreted protein, acidic, cysteine-	3.7
	448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77667	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	A227829	Hs.111882	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447336	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20840	3.6

5	450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease H1, large subunit	3.6
	417387	AW021102	Hs.21509	zf-C2H2:none	ESTs	3.6
	450825	AC005954	Hs.25527	PDZ,Guanylate_kdn;TM=N;SS	tight junction protein 3 (zona occi	3.6
	439755	AW748482	Hs.77873	ig;TM=Y;SS=M	B7 homolog 3	3.6
	439873	BE159253	Hs.300638		ESTs	3.6
	439039	AI556707	Hs.48713		ESTs	3.6
	419235	AA470411	Hs.288433	pkinaase:none	neurotrophin	3.6
10	445033	AV662402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	3.6
	404394	AF332975	Hs.307004	EGF,in1,vwc,vwd,MAM,Kerati	Zonadhesin	3.6
	452222	AW805287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
	422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
	420988	AW006352	Hs.159543		ESTs, Weakly similar to T32554 hypo	3.6
	430680	AW245741	Hs.58461	zf-C2H2,TFIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 knu	3.6
15	426815	D59505	Hs.351344	lg,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1CL_HUMAN	3.6
	437466	AA788946	Hs.101302	in3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
	421690	AW162667	Hs.106857	efhand;TM=M;SS=N	calbindin 2, (29kD, cake(nin)	3.5
	453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
20	426158	NM_001982	Hs.199067	Furin-like,kinase,Recep_	v-erb-b2 avian erythroblastic leuke	3.5
	439246	AI498072	Hs.351474	ank,kinase,UPF0073;TM=N;	membrane-associated tyrosine- and t	3.5
	410653	BE383768	Hs.65238	zf-C5HC4,AIP3;TM=M;SS=N	95 kDa retinoblastoma protein blnd	3.5
	412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
	427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
	444273	AI903474	Hs.230	LRR,LRRNT;TM=M;SS=M	fibromodulin	3.5
25	434936	AI285970	Hs.183817	UCH-2	ESTs	3.5
	457889	AJ077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
	422575	AK000546	Hs.118552	PTP2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
	428343	ALD43021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
	426716	NM_006379	Hs.171921	lg,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
30	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
	447041	AI135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
35	446945	AI193115	Hs.16611	TM=M;SS=N	tumor protein D52-like 1	3.5
	416322	BE019494	Hs.79217	PSGR,NAD_Gly3P_dh,Octopin	pyridine-5-carboxylate reductase 1	3.5
	447347	AA570066	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
	448984	AW751955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
	421778	AA428000	Hs.263072	NA;NA	actin related protein 2/3 complex,	3.5
40	423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
	432545	X52486	Hs.3041	cyclin:none	uracil-DNA glycosylase 2	3.5
	408495	W68796	Hs.237731		ESTs	3.5
	406851	AA609784	Hs.352392	lg,MHC_II_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
	418736	T18979	Hs.87908	helicase_C,AT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
45	410197	NM_005518	Hs.59889	HMG_CoA_synth;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
	453587	BE281130	Hs.33713	KH-domain,Fibronectin_S3_C,	myo-inositol 1-phosphate synthase A	3.4
	417259	AW903838	Hs.81800	EGF,lg,lectin_c,sushi,Xii	chondroitin sulfate proteoglycan 2	3.4
	453985	N4545	Hs.251865	PH:none	ESTs	3.4
	412634	U55984	Hs.355531		heat shock 90kD protein 1, alpha	3.4
50	407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
	444371	BE540274	Hs.239	Forik_head;TM=M;SS=N	forkhead box M1	3.4
	447334	AA515032	Hs.81109		ESTs	3.4
	426530	U24578	Hs.278625	A2M,MTR,ANATO,A2M_N,prexy	complement component 4A	3.4
	419749	X73508	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcv and kazal-l	3.4
55	423595	R82826	Hs.220702	homeobox:none	ESTs	3.4
	406673	M34996	Hs.198253	lg,MHC_II_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
	434241	AF118913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
	412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
	452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
60	431457	NM_012211	Hs.256287	FG-GAP,vwa;TM=Y;SS=M	Integrin, alpha 11	3.4
	421777	BE556208	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
	453082	H18835	Hs.31608	lon_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
	414085	AA114018	Hs.75745	aldedh;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
	440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
65	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	3.4
	433339	AF018226	Hs.8036	ras,arf;TM=M;SS=N	glioblastoma overexpressed	3.4
	419301	AA236166	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
	414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
70	451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
	432210	AI567421	Hs.273330	EGF,kazal,laminin_EGF,lam	Homo sapiens, clone IMAGE:3544662,	3.4
	452242	R50958	Hs.159993		glycosyltransferase	3.4
	450676	AI147155	Hs.279727		ESTs	3.4
	413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (aripapin 2)	3.4
	427919	AA173942	Hs.328416	CTF_NFI:none	Homo sapiens mRNA: cDNA DKFZp564H19	3.4
75	424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
	422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
	440995	T57773	Hs.10263		ESTs	3.4
	428150	NM_003658	Hs.187218	homeobox;TM=N;SS=M	BerH-like homeobox 2	3.3
80	416877	BE388286	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
	452191	AJ076408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
	450273	AW298454	Hs.24743	rrn:none	hypothetical protein FLJ20171	3.3
	456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
	423062	NM_003655	Hs.5537	chromo;TM=N;SS=M	ESTs	3.3
	421848	X15880	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

5	433577	AW007080	Hs.284192	Aa_trans;TM=Y;SS=N	ESTs	3.3
	409635	AA305729	Hs.18272	CTF_NFI:none	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	Sec7,PH,ANF_receptor,Ig_	Nuclear factor I/B	3.3
	422940	BE077458		trypsin;TM=M;SS=M	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
	410001	AB041036	Hs.57771	TM=Y;SS=M	kalikrein 11	3.3
	427461	AA531527	Hs.332040	TM=M;SS=N	hypothetical protein MGC13010	3.3
	453468	W00712	Hs.32990	HAT;TM=N;SS=M	DKFZP586F084 protein	3.3
	443807	W52930	Hs.9822		HCNP protein; XPA-binding protein 2	3.3
10	456034	AW450979			gb:U1-H-B13-ata-a-12-0-U1.s1 NCL CG	3.3
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
	412755	BE144306	Hs.179891	sugar_tr;Ribosomal_S25	ESTs, Weakly similar to P4HA_HUMAN	3.3
	429690	AW956329	Hs.23721	TM=M;SS=N	ESTs	3.3
	423472	AF041260	Hs.129057	perilipin;TM=N;SS=M	breast carcinoma amplified sequence	3.3
	424119	BE269041	Hs.140452	Frizzled,Fz	cargo selection protein (mannose 6	3.3
15	437275	AW976035	Hs.292396	TM=M;SS=N	ESTs, Weakly similar to A47582 B-ca	3.3
	437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3438		deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp586I133	3.3
20	451691	AB092878	Hs.208152	C2	ESTs	3.3
	430433	AA478883	Hs.273766	WW:none	ESTs	3.3
	429343	AK000785	Hs.199480	VHS,ENTH,UIM;TM=N;SS=M	Homo sapiens, Similar to epsk 3, c	3.3
	450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AB088490	Hs.248107	CN_hydrolase	ESTs, Weakly similar to ALU8_HUMAN	3.3
25	452579	AA131657	Hs.23830		ESTs	3.3
	409960	BE281944	Hs.355264		hexokinase 1	3.3
	408850	AB243000	Hs.172828	wvc;Collagen,COLF;TM=M;S	collagen, type I, alpha 1	3.3
	453874	AW591783	Hs.36131	homeobox:none	collagen, type XIV, alpha 1 (undull	3.2
	425864	AW869928	Hs.9071		progesterone membrane binding prote	3.2
30	428412	AA428240	Hs.126083		ESTs	3.2
	430316	NM_000875	Hs.239176	fn3,Furin-like,kinase,Pa	insulin-like growth factor 1 recept	3.2
	440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4,rm;	hypothetical protein FLJ22678	3.2
	449933	AW157098	Hs.324104	DUF176,efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	441128	AA570255	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
35	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	422737	M26939	Hs.119571	Collagen,COLF;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
	424971	AA479005	Hs.154036	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
	407869	AB27976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
40	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
	426991	AK001535	Hs.214410		Homo sapiens cDNA FLJ10674 fls, clo	3.2
	414081	AW969976	Hs.365706	gla;TM=N;SS=Y	matrix Gla protein	3.2
	408795	AW749128	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	3.2
45	437879	BE282082	Hs.5894	TM=N;SS=N	hypothetical protein FLJ10305	3.2
	407872	AB039723	Hs.40735	Fz,Frizzled,7tm_2,DUF81;T	frizzled (Drosophila) homolog 3	3.2
	427289	AB097346	Hs.323878	aminotran_5,SDF:none	phosphoserine aminotransferase	3.2
	432375	BE536069	Hs.2982	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
50	412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
	446942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
	439456	AB752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
	414774	X02419	Hs.77274	kringle,trypsin,plant_thl	plasminogen activator, urokinase	3.2
	433336	AF071986	Hs.31386	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 2	3.2
55	439905	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
	420251	AW374968	Hs.379829		Human DNA sequence from clone RP5-1	3.2
	413004	T35901	Hs.75117	TM=M;SS=N	interleukin enhancer binding factor	3.2
	418688	Z36830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
60	424391	BE550112	Hs.158549		ESTs, Weakly similar to T203_HUMAN	3.2
	440409	AW294316	Hs.125608	thioredo	ESTs	3.2
	452689	F33688	Hs.284176	transferrin,KH-domain,rm	transferrin	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4:none	nuclear receptor subfamily 1, group	3.2
	434384	AA831910	Hs.370133		ESTs	3.2
65	413436	AF238083	Hs.68061	DAGK;TM=M;SS=N	sphingosine kinase 1	3.2
	431663	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-iso protein	3.2
	432874	WB4322	Hs.279851	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
	436252	AB39519	Hs.142827		Homo sapiens cDNA FLJ11562 fls, clo	3.2
70	421044	AF061871	Hs.101302	fn3,wvc;Collagen,TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
	419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
	419359	AL043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast) hom	3.1
	441859	AW194364	Hs.9877	Amino oxidase,FAD_binding	interleukin-4 induced gene-1 protel	3.1
	428418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
	413076	U10564	Hs.75188	kinase;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
75	407874	AB766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fls, clo	3.1
	448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
	427024	AA387572	Hs.348902		chromosome 11 open reading frame 14	3.1
	410281	AF076612	Hs.166186	wvc,W2,MA3,MIF4G	Homo sapiens clone 23928 mRNA seque	3.1
80	447205	BE017015	Hs.11006	LEA,perilipin;TM=M;SS=N	ESTs, Moderately similar to T17372	3.1
	434433	AW629759			gb:hh70e05.y1 NCL_CGAP_GU1 Homo sap	3.1
	439737	AB751438	Hs.41271	C1q, Collagen, none	Homo sapiens mRNA full length inser	3.1
	450157	AW961578	Hs.60178	PH,Hand_41,RhoGEF,none	ESTs	3.1
	445989	H97754	Hs.11108		ESTs	3.1
	442213	N30110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1

	402496			PDZ;TM=N;SS=M	Target Exon
	438974	AF069816	Hs.6454	TM=N;SS=M	chromosome 19 open reading frame 3
	439335	AA742697	Hs.62492	MIF,sugar_tr,none	NM_052863:Homo sapiens secretoglobulin macrophage migration inhibitory factor dermatopontin
5	412276	BE262621	Hs.73798		ESTs
	416950	AL049798	Hs.80562	transmembrane4,none	SEC14 (S. cerevisiae)-like 2
	456157	AW979153	Hs.336881	CRAI1_TRIO,none	Immediate early response 3
	452753	AA028049	Hs.277778	TM=M;SS=N	KIAA1609 protein
10	414420	AA043424	Hs.76095	TM=M;SS=N	protein tyrosine phosphatase, receptor WD repeat domain 10
	446229	A1744964	Hs.14449	serpinf1;TM=N;SS=M	Homo sapiens cDNA: FLJ23260 fis, cl
	453143	AA382234	Hs.356289	WD40;TM=M;SS=N	hypothetical protein MGC3101
	411441	AL042365	Hs.70202	AAA,hormone_rec,zf-C4	transmembrane 4 superfamily member
	422921	BE062045	Hs.351625	IRK;TM=Y;SS=N	ESTs
15	444441	AW613841	Hs.301394	TM=Y;SS=M	ESTs
	436729	BE621807	Hs.351316	RFX_DNA_binding,none	ESTs
	427890	AA435761	Hs.373623	integrin_A_FG-GAP,none	ESTs
	444838	AV651680	Hs.208568		ESTs
	427876	AI84291	Hs.369171	Na_Ca_Ex;TM=Y;SS=M	sodium calcium exchanger
20	413040	AA193338	Hs.12321	EMP24_GP25L;TM=Y;SS=M	Integral type I protein
	427515	T79526	Hs.179516	filament;TM=N;SS=N	Homo sapiens mRNA for FLJ00074 prot
	451092	AI207256	Hs.13766	typseln,kingle,UPAR_LY6	ESTs
	422222	AI061301	Hs.164773		ESTs
	452813	AA401599	Hs.23459	SH3;TM=M;SS=N	SH3-domain binding protein 4
25	447191	NM_014521	Hs.17667	COX6C;TM=M;SS=M	cytochrome c oxidase subunit VIc
	412890	T85247	Hs.351875	TM=Y;SS=N	CGI-06 protein
	418313	BE244231	Hs.84038	AAA,NB-ARC,PAAD_DAPIN;NA;	NALP2 protein; PYRIN-Containing APA
	440006	AK000517	Hs.6844		Homo sapiens, Similar to tumor diff
	434042	AI589941	Hs.8254		KIAA1858 protein
	420576	AA297634	Hs.54925	pkinase,Sema,P81,TIG,A4_E	macrophage stimulating 1 receptor (
30	432269	NM_002447	Hs.2942		hypothetical protein C321D2.4
	424927	AW973666	Hs.153850	TM=M;SS=N	ESTs, Weakly similar to T2D3_HUMAN
	440100	BE382885	Hs.158549	TM=N;SS=N	hypothetical protein FLJ10687
	452408	AA306477	Hs.29379	zf-CCCH;TM=M;SS=N	RAD51 (S. cerevisiae) homolog (E co
	441362	BE614410	Hs.23044	Collagen;TM=Y;SS=N	radylate response factor 1 (EGF-res
35	418444	AB02889	Hs.85155	TM=M;SS=N	CSRF1 protein
	423464	NM_016240	Hs.128856	ras,none	KIAA1243 protein
	424604	AW865388	Hs.151076	LIM;TM=M;SS=N	RAS23, member RAS oncogene family
	420059	AF161488	Hs.94759	trypsin;TM=M;SS=N	ESTs
	453271	AA903424	Hs.6786	EGF,F5_F8_type_C;TM=N;SS=	kallikrein 10
40	411274	NM_002776	Hs.69423	ank;TM=M;SS=N	milk fat globule-EGF factor 8 prote
	434095	AA011117	Hs.3745	BTB,Pep_M12B_propept,Reprio	NM_031419:Homo sapiens molecule po
	403439			pkinase,F5_F8_type_C;TM=Y	kruppel-related zinc finger protein
	413244	AW955951	Hs.159285	LEA;TM=M;SS=N	discoiledin domain receptor family, m
45	411756	BE294360	Hs.71891	cadherin,Cadherin_C_term;	Homo sapiens mRNA; cDNA DKFZp434G08
	409007	AL122107	Hs.49599		adipose specific 2
	452547	AA335295	Hs.74120	TM=M;SS=N	cadherin 11, type 2, OB-cadherin (o
	414359	M62194	Hs.75929	MCPsignal,laminin_B,laminin	ESTs
	433212	BE218049	Hs.121820		KIAA0130 gene product
50	449123	D50920	Hs.23106		ESTs
	431176	AI026984	Hs.293662	WH1;TM=M;SS=N	ESTs
	419245	A1732742	Hs.87440	K-box;TM=N;SS=M	ESTs
	434433	AA635305	Hs.376591		ESTs
	449177	BE616694	Hs.288042	Cam_acyltransfer;TM=M;SS=N	hypothetical protein FLJ14299
55	430449	AA352723	Hs.241471	fn3,Ig;TM=Y;SS=M	RNB6
	452887	AI702223	Hs.107523	TM=M;SS=Y	hypothetical protein DKFZp761F241
	451678	AA374181	Hs.26759	TIC;TM=M;SS=N	DKFZP564D0764 protein
	454557	AF168793	Hs.12743	MATHz-zf-TRAF,zf-C3HC4;TM=	camitline O-octanoyltransferase
	407597	AA043825	Hs.339352	eIF5_eIF2B_W2;TM=M;SS=N	Homo sapiens brother of CDO (BOC) m
60	431829	AI077025	Hs.265827	zf-C3HC4;TM=Y;SS=M	Interferon, alpha-inducible protein
	432302	AA345857	Hs.274307		KIAA1442 protein
	425449	AI751601	Hs.8375		TNF receptor-associated factor 4
	437959	AI472068	Hs.375604		KIAA1856 protein
	447400	AK000322	Hs.18457		hypothetical protein FLJ20316
	411734	AW374954	Hs.71779	fn3,none	Homo sapiens DNA from chromosome 19
65	443547	AW271273	Hs.356487	TM=Y;SS=M	hypothetical protein FLJ12686
	417000	BE277919	Hs.306019	GTP_CDC;TM=N;SS=M	ESTs, Weakly similar to ALU7_HUMAN
	416887	D86957	Hs.80712	PIP5K;TM=N;SS=M	KIAA0202 protein
	424494	U78576	Hs.148255	pkinase,F5_F8_type_C,eth	phosphatidylinositol-4-phosphate 5-
	414496	W73863	Hs.355424	Occludin;TM=M;SS=N	ESTs
70	413335	AI569936	Hs.286178	ras,ark;TM=M;SS=N	hypothetical protein FLJ2637
	434314	BE382921	Hs.3797	TM=M;SS=N	RAS28, member RAS oncogene family
	401038			TM=Y;SS=M	C11000425:g[14507721]refNP_003310.
	418245	AA088767	Hs.83883	zf-C3HC4,Cbl_N,Cbl_N2,Cbl	transmembrane, prostate androgen in -
	407688	W26317	Hs.37616	TM=N;SS=N	Human O9 splice variant B mRNA, com
75	456906	AF117646	Hs.158637		Ces-Br-M (murine) ectopic retrovir
	424744	AW175781	Hs.152720		m-phase phosphoprotein 6
	452195	AA894712	Hs.116878		ESTs
	415988	BE407713	Hs.78943	Pep1_C1-like;TM=N;SS=M	bleomycin hydrolase
	418399	AF131781	Hs.84753	TM=N;SS=N	hypothetical protein FLJ12442
80	420568	F08247	Hs.247735	cadherin,tipocalin;TM=M;S	protocadherin alpha 10
	404861			TM=M;SS=N	C9000306:g[12737280]refXP_005682
	414152	NM_003248	Hs.75774	EGF,TSPN,bp_3;TM=M;SS=M	thrombospondin 4
	421307	BE539976	Hs.103305	chromo	Homo sapiens mRNA; cDNA DKFZp434B04
	444868	BE560471	Hs.12101	TM=N;SS=M	hypothetical protein

5	450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
	452864	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
	422105	AI929700	Hs.111680	TM=M;SS=N	endostatin alpha	3.0
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
	434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, clo	3.0
10	412678	NM_000166	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
	426801	AA486846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
	421983	AI252640	Hs.110364	pro_isomerase,none	peptidylprolyl isomerase C (cycloph	3.0
	428299	AI620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
	438746	AI885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

15 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

20	Pkey	CAT Number	Accession
	418344	245371_1	AA218387 T63548 AA228676
	412703	1243670_1	AW984759 AW984744
	434241	63414_1	AF119913 AI207698 R57074
25	422940	58443_1	BC012771 BG397153 BF366195 AA337277 AA319285 AW843252
	456034	685886_1	AA136653 AA136655 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	434433	111338_1	AA633408 AW749955 AW629759 AI651005

TABLE 4C

30 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

35	Pkey	Ref	Strand	Nt_position
	406387	9256180	Plus	116229-116371,117512-117651
	400496	9743564	Plus	41515-41695
40	402496	9797769	Minus	8615-9103
	403439	9719679	Plus	91463-91632
	401038	7232177	Minus	4277-4469
	404661	9797073	Plus	33374-33675,33769-34008

45 TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

50 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from Pfam (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: Ratio of 50th percentile tumor to 50th percentile of normal body tissue

55	Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGene Title	R1
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
60	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	13.7
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midline (neurite growth-promoting f	13.7
	414521	D20124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
	438091	AW373062	Hs.351548	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
65	413815	AL046341	Hs.75562	pklnase,F5_F8_type_C;TM=Y	discoilin domain receptor family, m	13.2
	439180	AI393742	Hs.199067	Furin-like,phkinase,Recep_	v-erb-b2 avian erythroblastic leuke	13.2
	431441	UB1961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.6
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
	452239	AW379378	Hs.356288		protein tyrosine phosphatase, recep	12.1
70	441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	11.9
	419223	X60111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
	413859	AW992356	Hs.8364	SAM_PWT,none	Homo sapiens pyruvate dehydrogenase	11.5
	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	10.1
75	419452	U33635	Hs.90572	lg,phkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
	427378	BE518037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
	444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
	436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
	412326	AI879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-r	9.5
80	425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxylkinase 1	9.5
	432638	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
	424208	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
	444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

5	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphatase 2B	9.0
	425932	AW886222	Hs.9973	SH2,WV,PID,none	lensin	8.9
	421143	AB024536	Hs.102171	ig_LRR,LRRT,LRRCT;TM=M;S	immunoglobulin superfamily containi	8.8
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
	410668	BE379794	Hs.159651	death,TNFR_c6;TM=Y;SS=M	hypothetical protein	8.7
	433662	W07162	Hs.150825	ras,ABC_tran,arf;TM=M;SS=	RAB25 RAB25, member RAS oncogene fa	8.6
	421853	AL117472	Hs.106924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
	425335	BE394327	Hs.296267	ethand,kazal,arf,ras,7tm_	folistatin-like 1	8.5
10	400290	H18636	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
	438089	W05391	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	8.4
	426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
	439941	AI392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
15	439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
	442213	N38110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
	412649	NM_002205	Hs.74369	integrin_A,FG-GAP;TM=M;SS	integrin, alpha 7	8.1
	448913	AA194422	Hs.22564	rm,zf-RanBP,pkinase,GST_	myosin VI	8.1
	420168	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
20	407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
	462516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
	443604	C03677	Hs.9515	ethand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
	429002	AW248439	Hs.2340	Amedillo_seg;TM=M;SS=N	junction plakoglobin	7.6
25	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
	426359	AA376409	Hs.10882	adenylatekinase,none	Homo sapiens cDNA: FLJ23313 fls, cl	7.5
	417733	AL048678	Hs.82503	NAANA	H.sapiens mRNA for 3'UTR of unknown	7.5
	451541	BE279383	Hs.26557	Amedillo_seg;TM=M;SS=N	plakophilin 3	7.4
	443951	F13272	Hs.358835	PMP22_Claudin,none	fennin, light polypeptide	7.4
30	409960	BE261944	Hs.356264		hexokinase 1	7.3
	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vwc	von Willebrand factor (VWF), mRNA	7.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
35	417771	AA804698	Hs.82547		retinoic acid receptor responder (t	7.0
	424118	BE289041	Hs.140452	parilin;TM=N;SS=M	cargo selection protein (mannose 8	7.0
	402705	X57951	Hs.180909	AtpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	417145	AW952792	Hs.334612	Sm,pkinase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
40	447216	R75812	Hs.169248	cytochrome_c;NA;NA	p75NTR-associated cell death execut	6.9
	422278	AF072873	Hs.114218	Fz,Fizzled,7tm_2;TM=Y;SS	fizzled (Drosophila) homolog 6	6.9
	414857	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (6.9
	447528	AI612027	Hs.76277	TB2_DP1_JHA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	6.9
	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
45	428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
	444143	AW747996	Hs.160999	Bcl-2,none	ESTs, Moderately similar to A58194	6.8
	414443	AIJ077268	Hs.76144	ig_pkinase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regula	6.7
	448479	H96115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acetylglucosamine pyrophospho	6.6
	410552	X06946	Hs.748	ig_pkinase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
50	414883	AA926960	Hs.348609	CXS;TM=N;SS=N	CDC28 protein kinase 1	6.6
	417426	NM_002291	Hs.82124	laminin_EGF,laminin_N1ema	laminin, beta 1	6.6
	428179	AI127772	Hs.279596	pkinase,PX,pkinase_C;TM=N	serum/glucocorticoid regulated kina	6.6
	443195	BE148235	Hs.193063	Aa_trans,none	Homo sapiens cDNA FLJ14201 fls, clo	6.5
	424512	X53002	Hs.149846	Integrin_B,EGF;TM=Y;SS=M	Integrin, beta 5	6.5
55	421733	AL119871	Hs.1420	ig_pkinase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
	428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
	450172	NM_006864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
	416078	AL034349	Hs.79006		protein tyrosine phosphatase, recep	6.5
	408912	AB011084	Hs.48024	Amedillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
60	428373	AI751658	Hs.183986	ig;TM=Y;SS=M	polliovirus receptor-related 2 (herp	6.4
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic; a	6.4
	406621	X57809	Hs.181125	ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
	431629	AJ077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
	428169	AI928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
65	443337	Y07604	Hs.9235	NDX;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
	451232	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	6.4
	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
	417208	867773	Hs.81665	ig_pkinase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
70	438278	BE408248	Hs.57988	TFIS,RNA_POL_M_16KD,UPFO	hypothetical protein FLJ22357 simil	6.3
	429455	AI472111	Hs.278694	lectin_c	CD209 antigen	6.3
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
	445033	AV52402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
	411756	BE294360	Hs.71891	pkinase,F5_F8_type_C;TM=Y	discolfin domain receptor family, m	6.3
75	453902	BE502341	Hs.3402		ESTs	6.3
	418005	AI186220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
	449924	W30681	Hs.145233	SH3,none	Homo sapiens cDNA: FLJ22130 fls, cl	6.2
	426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
	453064	R40334	Hs.89463		potassium large conductance calcium	6.2
80	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
	452683	AI089575	Hs.374574	homoobox,none	progesterone membrane binding prote	6.2
	402576	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
	444672	Z55636	Hs.11669	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
	450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

5	432314	AA533447	Hs.285173	Xlnk:none	ESTs	6.1
	438564	AA381553	Hs.198253	lg,MHC_IL_alpha,none	major histocompatibility complex, c	6.1
	442522	R21135	Hs.54985		ESTs	6.1
	425184	BE278288	Hs.155048	lg;TM=Y;SS=M	Lutheran blood group (Auberger b an	6.1
	431890	X17033	Hs.271986	wva,Integrin_A,FG-GAP;TM=	Integrin, alpha 2 (CD48B, alpha 2 s	6.1
	449475	A1348027	Hs.129825	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.1
	449538	A1559444	Hs.104679	TM=M;SS=M	ESTs	6.0
	414496	W73853	Hs.355424	pklnase,F5_F8_type_C,adh_	ESTs	6.0
10	414217	A1309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fis, cl	6.0
	445333	BE537841	Hs.44278	ras,arf;TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
	431183	NM_006855	Hs.250696	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
	409645	A1142265	Hs.55498	polypranyl_synt;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
	412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	5.9
15	416137	BE279513	Hs.278607	pklnase,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
	412969	A1373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
	414504	AW069181	Hs.116175	pklnase,SAM;TM=M;SS=N	sterile-alpha motif and leucine zip	5.9
	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,laminin	cadherin, EGF LAG seven-pass G-type	5.9
	436415	BE265254	Hs.343268	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
20	413900	AW409747	Hs.75612	TPR,PDZ,VW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
	441455	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc-finger regulated transporter-lik	5.9
	444005	BE395086	Hs.334762	ldl_recept_La,PKD,MHC_J;TM	type I transmembrane protein Fn14	5.8
	408269	AW888219	Hs.44077	Ch;TM=M;SS=N	parvin, alpha	5.8
	411372	A147861	Hs.213289	Glyco_transf_11,EGF,ldl_r	low density lipoprotein receptor (f	5.8
25	450825	AC005954	Hs.26527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona occi	5.8
	456534	AJ271671	Hs.100623	LIM,PDZ,pklnase;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
	451553	NM_001089	Hs.26830	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
	446812	AL042279	Hs.16206	pklnase	uncharacterized hypothalamus protei	5.7
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
30	406484	XM_093451		TM=N;SS=M	C3002124:gi12737280[ref]XP_008682	5.7
	425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
	444607	AW405635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.7
	421458	AW579842	Hs.104557	zf-C2H2,DUF18,efhand,C2_P	hypothetical protein FLJ10697	5.6
	412810	M21574	Hs.74615	lg,pklnase,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
35	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
	453880	A1803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	5.6
	439578	AW283124	Hs.350547	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
	450954	A1804740	Hs.25691	TM=Y;SS=M	receptor (calcitonin) activity mod	5.6
	414555	N98569	Hs.76422	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (plate	5.6
40	409963	AA133580	Hs.377830	MBOAT,none	calcium/calmodulin-dependent protei	5.6
	450463	AW852018	Hs.201398	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.6
	425177	AF127577	Hs.155017	TM=N;SS=M	nuclear receptor interacting protei	5.6
	445496	AB007860	Hs.12802	SH3,ank,PH,ArfGap;TM=M;SS	development and differentiation enh	5.6
	428961	BE313077	Hs.93135	mm	ESTs, Weakly similar to ALU2_HUMAN	5.5
45	424441	X14850	Hs.147097	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
	415862	AW972481	Hs.170610	pklnase,none	ESTs, Highly similar to G01887 MEK	5.5
	422105	A1929700	Hs.111680	TM=M;SS=N	endosulfine alpha	5.5
	429556	AW139309	Hs.314807	TM=M;SS=N	ESTs	5.5
	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	5.5
50	425205	NM_005854	Hs.155106	TM=Y;SS=N	receptor (calcitonin) activity mod	5.5
	444633	AF111713	Hs.12284	lg;TM=Y;SS=M	junctional adhesion molecule 1	5.5
	431565	AF161470	Hs.260622	TM=Y;SS=N	butyrate-induced transcript 1	5.5
	429055	U48959	Hs.211582	pklnase,fn3,lg,none	myosin, light polypeptide kinase	5.5
	431886	L77964	Hs.271980	pklnase;TM=M;SS=N	mitogen-activated protein kinase 6	5.5
55	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
	451863	AL120834	Hs.331803	cpn60_TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
	422293	X94453	Hs.114366	aldoh,asklnase;TM=M;SS=N	pyrroline-5-carboxylate synthetase	5.4
	432179	X75208	Hs.2913	EPH_bld,fn3,pklnase,SAM,T	EphB3	5.4
	408048	NM_007203	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PKA) anchor protein 2	5.4
60	448163	Y10805	Hs.20521	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
	421251	Z28913	Hs.102948	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
	439039	A1656707	Hs.48713	pklnase,none	ESTs	5.4
	409882	AJ243191	Hs.66874	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
	451295	A1557212	Hs.17132	pklnase,DAG_PE-bind,pklna	ESTs, Moderately similar to I54374	5.4
65	442549	A1751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
	445930	AF055009	Hs.13456	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
	453082	H18835	Hs.31608	lon_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
	426432	AF001601	Hs.168857	Arylesterase;TM=M;SS=N	paraoxonase 2	5.4
	415753	U52819	Hs.78781	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
70	450778	U81375	Hs.25450	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.4
	414739	U83867	Hs.77196	efhand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
	421233	AA209534	Hs.284243	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	5.3
	414774	X02419	Hs.77274	kringle,lypsin,plant_chi	plasminogen activator, urokinase	5.3
	414368	W70171	Hs.75939	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
75	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsm,z-al	ephrin-A3	5.3
	423819	T48691	Hs.249159	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
	440188	AK001812	Hs.7036	ROCK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
	414135	NM_004419	Hs.2128	Rhodanese,DSPe,Y_phosphat	dual specificity phosphatase 5	5.3
80	444838	AV651690	Hs.208559	integrin_A,FG-GAP,none	ESTs	5.3
	447918	A1129320	Hs.115175	pklnase,SAM,none	ESTs, Highly similar to JC5518 gamm	5.3
	405517	AF000974	Hs.119498	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.3
	413688	AA971014	Hs.75432	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
	411089	AA458454	Hs.355702		cell division cycle 2-like 1 (PITSL	5.2
	416157	NM_003243	Hs.342874	zona_pellucida;TM=Y;SS=M	transforming growth factor, beta re	5.2

5	407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
	448108	AL036595	Hs.42322	Paralemnin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2
	422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
	417098	AB017365	Hs.173859	Frizzled,Fz,7tm_2,loxin_2	frizzled (Drosophila) homolog 7	5.2
	430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
	414176	BE140638	Hs.75794	7tm_1,CRCB;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
	416710	AI268325	Hs.54890	Peptidase_M49,EGF,Ig,Neur	hypothetical protein FLJ23590	5.2
	417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
10	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	5.2
	421837	AF135168	Hs.108802	AAA,cdc48_N,cdc46_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
	429379	NM_014840	Hs.200598	kinase,RIOT;TM=M;SS=N	KIAA0637 gene product	5.2
	429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
	437275	AW976035	Hs.282386	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ae	5.1
15	421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHU1E colt	5.1
	448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
	452568	AA805534	Hs.300870	PI3_PIA_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
	452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
	437175	AW968078	Hs.87773	pk kinase, pk kinase_C, none	protein kinase, cAMP-dependent, cat	5.1
20	437056	AI147081		spectrin,SH3,PH,CH	gbork33af1.s1 Scores_NSF_FR_9W_OT_P	5.1
	450998	BE387614	Hs.25797	rm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kD	5.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
	448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	5.1
25	443412	WB4893	Hs.9305		angiotensin receptor-like 1	5.1
	412853	M34175	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
	439866	AA280717	Hs.6727	rm,NTF2;TM=M;SS=N	Res-GTPase activating protein SH3 d	5.1
	439975	AW328081	Hs.6817	Ham1p,like;TM=M;SS=N	Inosine triphosphatase (nucleoside	5.1
	435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
30	433423	BE407127	Hs.8997	HSP70,Ig,Ppx-GppA;TM=M;SS	heat shock 70kD protein 1A	5.1
	412641	M16680	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kD protein 1, beta	5.1
	431236	AV556840	Hs.285115	fn3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1
	438552	AJ245820	Hs.6314		type I transmembrane receptor (seiz	5.0
	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
35	427502	AI811865	Hs.7133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
	414166	AW888941	Hs.75789	DEAD,helicase_C,rm,Ndr,C	N-myc downstream regulated	5.0
	424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0
	422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFRA_HUMAN	5.0
	426836	BE242834	Hs.2055	THF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
40	410793	AW581906	Hs.66392	SH3,effhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

45	Key:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
	Key	CAT Number Accession
50	437056	428504_3 AW976398 AI147061 AA766223 AA743380 AI803927

TABLE 5C

55

Play:
Ref:
Strand:
NL_position:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

60

Play	Ref	Strand	NL_position
405484	5922025	Plus	199214-199579,189672-199920,200282-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75	Key:	Unique Eos probeset identifier number
	ExAcn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	25.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
10	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.50
	444783	AK001468	Hs.82180	anillin (Drosophila Scraps homolog), act	21.16
	415989	AI267700	Hs.317584	ESTs	20.95
15	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
	421470	R27498	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
20	450531	AW301032	Hs.203800	ESTs	16.60
	432867	AW016936	Hs.233364	ESTs	16.35
	443211	AI128388	Hs.143656	ESTs	15.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	405964	M21305		gb:Human alpha satellite and satellite 3	15.00
25	410355	S58544	Hs.153057	sperm associated antigen 1	14.70
	441377	BE218239	Hs.202556	ESTs	14.45
	413318	AU076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
	440304	BE159984	Hs.125395	ESTs	14.25
30	426427	M86699	Hs.169840	TTK protein kinase	13.60
	451561	N52812	Hs.177403	ESTs	12.80
	434032	AW005951	Hs.208892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	12.55
35	428684	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
	446282	AI281848	Hs.194691	retinoic acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosoph	11.85
	419752	AA249573	Hs.152818	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
40	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
	452461	N78223	Hs.108106	transcription factor	11.42
	431868	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400534				11.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
45	453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
	425890	AA393187	Hs.41294	ESTs	10.60
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.15008	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
50	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp584F093 (fr	10.40
	425761	AW684214	Hs.196729	ESTs	10.25
	404567				10.15
	428536	AI143139	Hs.2288	visfakin-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
55	453504	BE514127		gb:G01316974F1 NIH_MGC_8 Homo sapiens cD	9.95
	458018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE378594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	9.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
60	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
	420900	AL045633	Hs.44289	ESTs	9.68
	438639	AI278360	Hs.31409	ESTs	9.55
	439521	AI808955	Hs.58248	ESTs	9.55
	445676	AI247763	Hs.18928	ESTs	9.50
65	408489	AI082437	Hs.26690	ESTs	9.50
	418738	AW388833	Hs.6682	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.98
	400195	NA		NA	8.90
70	411765	H43348		gb:yp09a04.r1 Soares breast 3NblHst Homo	8.90
	418895	AA894638	Hs.14800	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
75	414559	AV856184	Hs.76452	C-reactive protein, pentraxin-related	8.64
	445436	AI224105	Hs.151408	ESTs	8.50
	403776				8.50
	433447	U29195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
80	419335	AW960146	Hs.284137	hypothetical protein FLJ12688	8.30
	422505	AL120862	Hs.124165	ESTs	8.25
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8483	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443460	N66045	Hs.133629	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44804	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AJ697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
15	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23820	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23485	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
20	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	7.15
25	421373	AA806229	Hs.167771	ESTs	7.10
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.126845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203863	hypothetical protein FLJ10339	6.95
30	413573	AI733859	Hs.149089	ESTs	6.85
	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586M1518 (f	6.82
35	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23155 fis, clone L	6.80
	453102	NM_007197	Hs.31684	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
	401644				6.70
	450434	AA166960	Hs.185870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
45	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423686	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	AA121886	Hs.10592	ESTs	6.47
	406871	AA129547	Hs.285764	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001828	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI087560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AI005457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-es	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407746	AK001952	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172886	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	418857	AA188775	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisia	6.16
	420096	AA775910	Hs.95011	synthrophin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.11
	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172406	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

5	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
	412245	AI160873	Hs.69233	zinc finger protein	5.96
10	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	416421	AA134008	Hs.79306	eukaryotic translation initiation factor	5.95
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
15	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	409908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
20	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypothet	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	408687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
25	459309	AA040820	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
30	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949952	Hs.49397	ESTs	5.75
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
35	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
	433687	AA743891		gb:ny57g01.e1 NCL CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
40	452608	M45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
	451177	AI969716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
45	436217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA138593	Hs.1975	hypothetical protein FLJ21007	5.55
	426235	AI631894	Hs.34447	ESTs	5.55
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 (Hsapi	5.53
50	444743	AA045648	Hs.301957	nucleic acid (nucleoside diphosphate linked mo	5.52
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004896	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
55	419502	AI076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
	441421	AA356782	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
60	428046	AW812795	Hs.165381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
	409554	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AI428056	Hs.23921	hypothetical protein DKFZp547A023	5.35
65	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	416139	AW975942	Hs.48524	ESTs	5.30
	421140	AA219891	Hs.73625	RABG interacting, kinesin-like (rakkinas	5.29
	424086	AI351010	Hs.102287	lysyl oxidase	5.27
70	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycidamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
	449347	AV849748	Hs.295901	KIAA0493 protein	5.25
75	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453821	AI824009	Hs.44577	ESTs	5.25
	413582	AW295847	Hs.71331	hypothetical protein MGC5350	5.25
	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
	407884	BE075316	Hs.95011	synaptobin, beta 1 (dystrophin-associated	5.24
80	433384	AI021892	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ13046	5.20
	441795	N58115	Hs.21137	AD024 protein	5.20
	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137516	fdgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

5	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79983	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
	447713	AI420733	Hs.207083	ESTs	5.15
10	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
	441139	AW449009	Hs.126647	ESTs	5.13
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
15	436202	AI974313	Hs.170204	KIAA0551 protein	5.10
	431689	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
	422805	AA436889	Hs.121017	H2A histone family, member A	5.07
	411750	BE562298	Hs.74827	KIAA0112 protein; homolog of yeast ribos	5.06
20	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
	415091	AL044872	Hs.77810	3-hydroxy-3-methylglutaryl-Coenzymes A sy	5.05
25	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA		NA	5.00
	408562	AA36323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
30	414718	H95348	Hs.107987	ESTs	4.91
	419139	AI123617	Hs.268940	ESTs	4.90
	430789	AA832577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	4.90
	425420	BE535911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
35	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224861	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
	450588	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN 9	4.87
40	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.87
	421128	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
	418395	AI765805	Hs.26691	ESTs	4.85
	430510	AW162916	Hs.241576	hypothetical protein PROC2577	4.84
45	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA		NA	4.70
50	451807	W52854	Hs.27089	hypothetical protein FLJ23293 similar to	4.68
	436882	AI582393	Hs.126885	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
55	417860	AW408557	Hs.235488	hypothetical protein FLJ14075	4.65
	410558	AW105231	Hs.182035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
	438397	AA715013	Hs.169836	ESTs	4.60
60	439225	AA182669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
	412723	AA648459	Hs.335951	hypothetical protein AF301222	4.59
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
65	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121888	ESTs, Moderately similar to PC4259 ferri	4.55
70	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324543	Hs.246106	ESTs	4.55
	416467	H57585	Hs.37467	ESTs	4.55
	408867	AA437199	Hs.656	cell division cycle 25C	4.54
	419423	U26488	Hs.90316	KIAA0007 protein	4.54
75	414132	AI801236	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.263077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	4.50
	451009	AA013140	Hs.115707	ESTs	4.50
	431064	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
80	432725	AI137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
	410486	AW235094	Hs.69233	zinc finger protein	4.50
	429532	AF157326	Hs.184786	TBP-Interacting protein	4.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408380	AF123050	Hs.44532	ubiquitin	4.49
	423936	U77629	Hs.135639	actin-like scute complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypothe	4.45
	410142	AA081824	Hs.124918	KIAA1795 protein	4.46
5	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	A1016377	Hs.131693	ESTs	4.41
10	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
	429774	A1522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.126355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284966	Hs.266308	mosaic serine protease	4.40
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	A1796376		gb:b34507.x1 NCL CGAP_Cv23 Homo sapiens	4.37
	448306	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410566	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
	459674	A1741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
20	448243	AW369771	Hs.52620	integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	A1292036	Hs.150028	ESTs	4.34
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
25	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422836	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA652985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothe	4.30
30	458076	R80081	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413861	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW885757	Hs.257862	ESTs	4.26
	417956	AA210704	Hs.190465	ESTs	4.26
	458433	AL136352	Hs.265883	ESTs, Weakly similar to I38022 hypothe	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.24
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
40	424583	AF017445	Hs.150926	fructose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like	4.20
	446912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	A1005888	Hs.134779	EST	4.20
45	411893	R82845	Hs.273789	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	A1793163		gb:cn52g03.y5 NCL CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	418229	A1827237	Hs.262884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcolemma-associated protein	4.16
55	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	A372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA161520	Hs.334822	hypothetical protein MGC4486	4.15
	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	A1798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	crossomucoid 1	4.10
65	440209	H10049	Hs.22269	neurexin 3	4.10
	435148	A918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167631	methylcrotonoyl-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothe	4.10
70	444188	A1393165	Hs.689	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rnp40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasia 1, anhydrotic receptor	4.09
75	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63831	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434062	A1373481	Hs.137175	hypothetical protein PRO1777	4.05
	443646	A1085198	Hs.164226	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23069 fis, clone L	4.05
	418624	AA300576	Hs.85789	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tra	4.05

5	447207	AAA42233	Hs.17731	hypothetical protein FLJ12892	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
	424176	AL137273	Hs.142307	hypothetical protein	4.04
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.04
10	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
	449448	D60730	Hs.57471	ESTs	4.00
15	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316			4.00
	408155	AB014528	Hs.43133	gb:tm26n09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	413841	M34276	Hs.75576	KIAA0628 gene product	4.00
	400110	NA		plasminogen	3.98
20	400289	X07820	Hs.2258	NA	3.98
	443715	AI583187	Hs.9700	matrix metalloproteinase 10 (stromelysin	3.97
	408296	AL117452	Hs.44155	cyclin E1	3.97
	450164	AI239923	Hs.30098	DKFZP586G1517 protein	3.97
	451592	AI805416	Hs.213897	ESTs	3.97
25	402373	AL135225	Hs.301865	ESTs	3.95
	426199	AA371865	Hs.97090	dopachrome tautomerase (dopachrome delta	3.95
	414148	BE084049		ESTs	3.95
	417008	AW673506	Hs.80758	gb:PMO-BT0651-270400-003-02 BT0651 Homo	3.95
	449532	W74653	Hs.271593	aspartyl-tRNA synthetase	3.94
30	434651	BE387182	Hs.280858	ESTs, Moderately similar to A47582 B-cel	3.93
	436291	BE568452	Hs.5101	ESTs, Highly similar to A35661 DNA excis	3.93
	423337	NM_004655	Hs.127337	protein regulator of cytokinesis 1	3.92
	416185	AW975861	Hs.47367	axin 2 (conductin, axil)	3.91
	443054	AI745185	Hs.8939	KIAA1785 protein	3.91
35	432596	AJ224741	Hs.278481	yes-associated protein 65 kDa	3.90
	451229	AW967707	Hs.48473	matrilin 3	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
	432702	AW973953	Hs.293744	ESTs	3.90
	437207	T27503	Hs.15829	hypothetical protein FLJ12910	3.90
40	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fls, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp434B0328 (I	3.90
	428622	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
	432289	AI860145	Hs.55118	ESTs	3.89
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
45	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11680 fls, clone HE	3.88
	410094	BE147897	Hs.53593	general transcription factor IIF, polype	3.88
	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
	444059	R69743	Hs.116774	Integrin, alpha 1	3.86
50	428282	AI782141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
	454403	BE065985		gb:RC3-BT0319-120200-014-s09 BT0319 Homo	3.85
	448315	AW290912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	3.85
55	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276690	Hs.146086	ESTs	3.83
	449508	AK001566	Hs.23818	hypothetical protein FLJ10704	3.82
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
60	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
	431716	D85053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
	437631	AA784749	Hs.287245	hypothetical protein FLJ14803	3.80
65	429118	H20569	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450096	AW682088	Hs.79357	holocarboxylase synthetase (biotin-prop	3.80
70	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423681	AK001720	Hs.134409	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.76
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
75	420725	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48696 cell prol	3.73
	443354	AW970572	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
	406667	M12523	Hs.184411	albumin	3.72
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
80	417246	AI760098	Hs.21411	ESTs	3.72
	410864	NM_008093	Hs.65370	lipase, endothelial	3.71
	432836	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fls, clone NT	3.70
	442881	AI023175	Hs.167022	ESTs	3.70
	432355	AA831032	Hs.111670	ESTs, Highly similar to JC2257 protyl of	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

5	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.69
	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
10	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
	417791	AW985339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.65
15	432023	AW273128	Hs.330144	EST	3.66
	430294	A1538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
	420596	AA278865	Hs.88523	ESTs	3.65
	404477	NA	NA	NA	3.65
20	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE168006	Hs.212296	ESTs	3.65
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
	457465	AW301344	Hs.122508	DNA replication factor	3.64
25	438149	A1754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
	424841	AB001108	Hs.151413	gila maturation factor, beta	3.63
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.62
30	411975	A1916058	Hs.144583	ESTs	3.61
	408239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429628	H09604	Hs.13268	ESTs	3.61
	449722	BE280074	Hs.23980	cyclin B1	3.60
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheli	3.60
35	419945	AW290975	Hs.118923	ESTs	3.60
	410365	A1287518	Hs.82669	Homo sapiens mRNA; cDNA DKFZp566D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
40	427943	AW969075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028892	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
	418688	T85017	Hs.1192	KIAA0074 protein	3.59
	436961	AW375974	Hs.156704	ESTs	3.58
45	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	NS8650	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
	401165	NA	NA	NA	3.55
50	415382	A1743539	Hs.72485	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421628	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
	443325	BE398008	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.181621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
55	450715	A1265484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily 11E (ethanol-	3.55
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
	434206	AW136873	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.54
60	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.52
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
	452940	AA029722	Hs.21773	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
65	440400	AA994364	Hs.125594	ESTs, Weakly similar to T26472 hypotheti	3.50
	453439	A1572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW389351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.48
	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukemia	3.47
	427975	A1536056	Hs.122460	ESTs	3.46
70	400297	A1127078	Hs.334473	hypothetical protein DKFZp564O1278	3.45
	404253				3.45
	435557	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.45
	417315	A1080042	Hs.336901	ribosomal protein S24	3.45
75	419140	A1882647	Hs.215725	ESTs	3.44
	446901	A1347274		gb:to05d02x1 NCL_CGAP_Co16 Homo sapiens	3.43
	461806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
	411571	AA122993	Hs.70811	hypothetical protein FLJ20516	3.42
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
80	443428	AF098168	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.41167	ESTs	3.41
	430264	AA470519		gb:nc71f10.s1 NCL_CGAP_Pr1 Homo sapiens	3.40
	450159	A1702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JC5795 CDEP prot	3.40
	444828	A1674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.102290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW630803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.86617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
5	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AI969703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	3.38
10	446432	AI377320	Hs.150058	ESTs	3.36
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cutlin 5	3.35
15	407819	R42185	Hs.274803	ESTs	3.35
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35
20	454018	AW016892	Hs.100855	ESTs	3.35
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW951186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW281488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
25	438008	AA775026	Hs.203802	ESTs	3.33
	421248	AW582962	Hs.102897	CGI-47 protein	3.33
	451707	AW051091	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349.1 HSPC0	3.31
30	443613	AI079356		gbvz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.31
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.31
	438746	AI865815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30
	427738	NM_000318	Hs.180812	peroxisomal membrane protein 3 (3SKD, Ze	3.30
	458855	AW351299	Hs.107000	hypothetical protein FLJ11294	3.30
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
	424770	AA425562	Hs.11065	Homo sapiens HDOME13P mRNA, partial ods	3.30
	417720	AA205625	Hs.208057	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8667	ESTs	3.28
40	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.28
	437222	AL117588	Hs.12778	ESTs	3.28
	422655	AJ011812	Hs.119018	transcription factor NRF	3.28
	414706	AW340125	Hs.78989	KIAA0097 gene product	3.28
	446665	D13767	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
45	447829	AI433029	Hs.164104	ESTs	3.27
	427676	BE242811	Hs.2173	fucoyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gbvz35f03.r1 NCL_CGAP_Bi5 Homo sapiens	3.26
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
50	424581	M62082	Hs.150917	catenin (cadherin-associated protein), a	3.25
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypotheti	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.25
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
55	410659	AI080175	Hs.68825	ESTs	3.25
	446202	AI279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439262	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
60	441264	AA927170	Hs.23290	ESTs	3.25
	424061	NM_008413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	cortisolem	3.24
	447432	AW968473	Hs.301957	radix (nucleoside diphosphate linked moi	3.24
	404519				3.24
65	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
70	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
	426472	BE246138	Hs.30853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB5 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
75	443162	T49851	Hs.9029	DKFZP434G032 protein	3.20
	431678	AW072372	Hs.287446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241428	DKFZP434B051 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypotheti	3.20
80	434180	BE551198	Hs.114275	ESTs	3.20
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412966	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haploglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S84054 hypotheti	3.18

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889882	Hs.271826	ESTs, Weakly similar to I38022 hypothetical	3.17
5	429616	AI982722	Hs.120845	ESTs	3.17
	415083	AK532683	Hs.27179	Homo sapiens cDNA FLJ12833 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B)	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423628	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
10	443830	AI142095	Hs.143273	ESTs	3.15
	413516	BE145807		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
15	427687	AW003887	Hs.1570	histamine receptor H1	3.15
	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	3.15
	445821	AW015211	Hs.146181	ESTs	3.15
20	429957	AW204530	Hs.99500	ESTs	3.15
	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
	439277	R80061	Hs.164447	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406688	T62745	Hs.184411	albumin	3.13
	452194	AK694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420811	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE3448343, mRNA,	3.11
35	441790	AW294809	Hs.132208	ESTs	3.11
	439352	BE614347	Hs.168615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU 6	3.10
	424602	AK002055	Hs.161046	hypothetical protein FLJ11193	3.10
40	402963				3.10
	428987	AW878441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (zf-znf1) m	3.10
45	426853	U52974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420817	AK001852	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908187	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
50	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.10
	433037	NM_014158	Hs.279938	HSPC067 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AJ217477	Hs.194591	ESTs	3.09
	415786	AW418198	Hs.257924	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axin 2 (conductin, axl)	3.08
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290838	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORT1	3.07
	443323	BE660621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119899	hypothetical protein FLJ12869	3.07
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384882	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M82248	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA161342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pennexin 1	3.06
	447048	AW383080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	3.05
70	406333				3.05
	428454	U55936	Hs.184378	synaptosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RC0-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
75	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	3.05
	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, fetal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

5	419185	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
	446861	A1696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.02
	452834	A1638627	Hs.105686	KIAA1668 protein	3.02
	410192	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
	416568	H04044	Hs.136558	ESTs	3.02
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
10	412719	AW016610	Hs.129911	ESTs	3.01
	438588	AA922836	Hs.110039	ESTs	3.01
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
	429703	T93154	Hs.28705	ESTs	3.00
	400296	AA305627	Hs.139338	ATP-binding cassette, sub-family C (CFTR	3.00
15	415261	T40928	Hs.8346	ESTs	3.00
	419435	A1200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
	429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
	407182	AA312551	Hs.230157	ESTs	3.00
20	424202	BE350295	Hs.15032	RAN binding protein 17	3.00
	444585	AW170015	Hs.6594	ESTs	3.00
	420552	AK000492	Hs.88808	hypothetical protein	3.00
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
	441928	A1370188	Hs.211454	ESTs	3.00
25	430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
	417806	A1867277	Hs.183733	ESTs	3.00
	447175	A1365208	Hs.293608	ESTs	3.00
	417177	NM_004458	Hs.81452	fatty-acyl-Coenzyme A ligase, long-chain	3.00
30	435447	A1872932		gb:wm72e03.x1 NCI_CGAP_U12 Homo sapiens	3.00
	406394				3.00
	454875	AW848047		gb:U3-CT0214-291289-052-A12 CT0214 Homo	3.00
	441635	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

TABLE 6B

	Pkey:	Unique Eos probeset identifier number		
40	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
Pkey	CAT number	Accession		
45	411785	125700_1	H43346 AA248302 AA095182	
	411864	1262055_1	AW848147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160	
	412359	129085_1	AW837985 AW837938 AA101955 AW837913 AW837935	
	413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856	
	414148	142133_1	BE084049 AW282907 AA135884	
50	424492	240008_1	A133482 A1207619 AA341625	
	430264	315008_1	AA470519 BE303010 BE302854 BE384120	
	431084	327472_1	A1903735 AA491283 A1694953 AW976903 AA761362	
	433687	373061_1	AA743991 AA604852 AW272737	
55	434414	38585_1	A1798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218667 AA055556 AW858231	
			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139	
			AA149776 AA699829 AW879188 AW813567 AW813538 A1267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730	
			AA157715 AA053524 AW848581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE158909 AA226824 A1829309 AW991957	
			N66551 AA527374 H66215 AA045564 A1694265 H68008 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659	
			BE081531 H69570	
60	435447	406400_1	A1872932 AA682306 BE220163 WB8695 TB1307 H91447	
	436411	419334_1	AW674352 AA715374 Z25205	
	443813	575391_1	A1079358 W23287	
	446901	697809_1	A1347274 AW844024	
	448310	757918_1	A1480316 AW847535	
65	451401	868474_1	A1793163 AW875182 AW875178 AW875176	
	454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066083	
	454975	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905	
			AW848214	
70	455838	1374606_1	BE145808 BE145807 BE181883	

TABLE 6C

75	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:469-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		

	Pkey	Ref	Strand	Nt_position
5	400534	6981826	Minus	278637-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401644	8576138	Plus	82855-83959
	401823	2262095	Minus	42575-42697,43189-43287,45830-45974
10	402167	8571795	Plus	109122-110367
	402983	5419653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770611	Minus	1414-1513,1624-1756
	404026	7341444	Plus	131740-131905
15	404232	8218045	Minus	71800-71956
	404253	9367202	Minus	55675-56055
	404477	8080699	Plus	113390-113577
	404516	8151967	Plus	114153-114322
	404519	8152000	Plus	12817-13000
20	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40567-40674,42351-42450
	405394	6624123	Minus	31900-32373
	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
25	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49593-49850

30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35	Pkey:	Unique Eos probe set identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
45	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1193 protein	49.18
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
50	429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
	452281	T93600	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
	447033	AI957412	Hs.157601	ESTs	31.24
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	28.84
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
55	413841	MS4276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	408906	AW847814	Hs.289305	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415899	AI267700	Hs.317584	ESTs	20.92
60	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
	421470	R27496	Hs.1378	annexin A3	17.92
	424051	AI110203	Hs.139411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
	439759	AI358055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AA046573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
65	421462	AF016495	Hs.104524	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30698	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gln:21d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
	433447	U29195	Hs.3281	neuronal pentraxin II	16.59
70	414386	X00442	Hs.75990	haploglobin	16.19
	425260	L47726	Hs.1870	phenylethylamine hydroxylase	16.08
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W78326		gl:zd50d04.r1 Soares fetal heart_Nb1H19W	15.80
	443211	AI128388	Hs.143655	ESTs	15.78
75	438608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414559	AV66184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412718	AW016610	Hs.129911	ESTs	15.24
	439451	AF086270	Hs.278664	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

5	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	A1767056	Hs.193002	ESTs	14.30
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, I2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
10	433213	AW666130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AAB11244	Hs.164168	ESTs	13.40
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673606	Hs.807588	aspartyl-tRNA synthetase	13.00
15	449199	A1990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AH33452	Hs.75431	fibrinogen, gamma polypeptide	12.83
	451581	N52812	Hs.177403	ESTs	12.72
	420734	AW972872	Hs.293736	ESTs	12.70
20	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	12.50
	441377	BE218239	Hs.202658	ESTs	12.45
	435981	H74318	Hs.188620	ESTs	12.38
	417296	L36196	Hs.81884	autotransferase family, cytosolic, 2A,	12.38
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
25	459370	AA869982	Hs.271826	ESTs, Weakly similar to I38022 hypothe	12.34
	430290	A1734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
	450628	AW382884	Hs.204715	ESTs	12.24
	446232	A1281848	Hs.194691	retinoic acid induced 3	12.16
30	428223	AA424313	Hs.98402	ESTs	12.08
	432582	A1823817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	12.02
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	N58172	Hs.109370	ESTs	11.84
35	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	11.68
	447532	AK000814	Hs.18791	hypothetical protein FLJ20607	11.67
	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
40	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
	452903	A1953425	Hs.246911	ESTs, Weakly similar to I38022 hypothe	11.32
	439011	H07860	Hs.306044	CGI-05 protein	11.30
45	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44080	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
50	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251945	poly(A)-binding protein, cytoplasmic 1-I	10.68
	440528	A1832243	Hs.211471	ESTs	10.63
	427644	A1767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	10.62
55	447974	R76886		glycyl64b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053308	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
	457065	A1476318	Hs.192480	ESTs	10.40
	408950	AA207814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
60	418852	AW503756	Hs.286184	hypothetical protein U551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447505	AL049288	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.28
	404567				10.14
	428536	A1143139	Hs.2288	visinin-like 1	10.08
65	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	10.05
	437267	AW511443	Hs.268110	ESTs	10.00
	420583	H77859	Hs.85450	reticulin 4	10.00
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013589	Hs.164424	deiodinase, iodothyronine, type II	9.97
70	449555	A1021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:yi80c11.r1 Soares placenta Nb2HP Homo	9.90
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14248 fis, clone OV	9.84
75	448106	A1800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446819	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
	440591	AA431559	Hs.132799	hypothetical protein FLJ23451	9.44
80	440404	A1015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.38
	401742	NA		NA	9.30
	416393	N54037	Hs.262668	plasminogen-like	9.28
	413339	A1818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL060050	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149796	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419968	X04430	Hs.93913	Interleukin 6 (interferon, beta 2)	9.18
5	413597	AW302895	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
10	450164	AI239923	Hs.30098	ESTs	8.95
	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140396	Hs.21821	hypothetical protein DKFZp762C076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW638616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	8.90
	419131	AA406293	Hs.41167	ESTs	8.86
15	444783	AK001488	Hs.62180	anilin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
20	419762	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
	412446	AI768015	Hs.92127	ESTs	8.71
	433285	AW975944	Hs.237396	ESTs	8.68
	414538	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
	430835	AI240006	Hs.192326	ESTs	8.60
25	445467	AI239832	Hs.15817	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256462	Hs.2257	vitronectin (serum spreading factor, som	8.50
	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
30	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA233056	Hs.191518	ESTs	8.42
	445436	AI224105	Hs.151408	ESTs	8.38
35	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	8.34
	425781	AW664214	Hs.196729	ESTs	8.33
	448419	R34810	Hs.119172	ESTs	8.29
40	407007	U22961		gb:Human mRNA clone with similarity to L	8.28
	420900	AL046633	Hs.44269	ESTs	8.25
	452503	AB000508	Hs.29736	TNF receptor-associated factor 5	8.23
	456242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:AF76g11.s1 NCL_CGAP_Cc3 Homo sapiens	8.16
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
	446155	AA558595	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	418379	AA218940	Hs.137616	hedgehog-like 1	8.07
	424560	AA158727	Hs.160555	protein predicted by clone 23733	8.06
	453116	AI276680	Hs.146088	ESTs	8.04
50	419929	U90288	Hs.93810	cerebral cavernous malformations 1	8.04
	409687	T51125	Hs.8493	ESTs	8.00
	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14886 fis, clone PL	8.00
	416681	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37975	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AI031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
	421833	AF121880	Hs.106260	sorting nexin 10	7.92
	432542	AW083920	Hs.16098	claudin 2	7.86
	414869	AA157291	Hs.21479	ubiquitin 1	7.84
60	419502	AJ076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V00495	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	439516	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
	406360	NA		NA	7.76
65	406887	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112284	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N68045	Hs.133528	ESTs	7.70
	449870	AJ672487	Hs.15423	hypothetical protein H0CMC04P	7.64
70	425681	AB018297	Hs.158183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AI301918	Hs.334284	ESTs	7.60
	420807	AA280627	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
	410718	AI920783	Hs.191435	ESTs	7.60
75	430848	AW021726		gb:AF227e02.y1 Morton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4269 ferri	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
	458897	AW937420	Hs.69662	ESTs	7.54
80	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50986	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445640	AW989626	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	7.49
	404596				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
5	431193	AW749505	Hs.296770	KIAA1719 protein	7.43
	413630	AA130158	Hs.19977	ESTs, Moderately similar to ALUJ8_HUMAN A	7.40
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
10	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
15	445019	AK205540	Hs.281295	ESTs	7.28
	419474	AW888619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gbyp09a04.r1 Soares breast 3NBH8st Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
20	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.18
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.78177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
25	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
	448705	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
30	439295	AW206091	Hs.253536	ESTs	7.08
	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431766		gbzw80c03.s1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
35	432435	BE218886	Hs.282070	ESTs	7.05
	427833	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
40	446322	N23033	Hs.155814	ESTs	6.98
	442577	AA292998	Hs.183900	ESTs	6.98
	429496	AF156827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA448854	Hs.271004	ESTs, Weakly similar to 138022 hypotheti	6.90
	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05788	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
50	424402	M63108	Hs.1769	lutalizing hormone/choriogonadotropin r	6.86
	433694	BE379823	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419829	AB020895	Hs.91662	KIAA0888 protein	6.80
55	451685	AA058246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	448501	AI302616	Hs.150819	ESTs	6.78
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
60	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418556	AM17215	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31684	frizzled (Drosophila) homolog 10	6.62
	433615	AA732982	Hs.269807	ESTs, Weakly similar to ALU1_HUMAN ALU 8	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF046586	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.22958	Homo sapiens clone IMAGE451939, mRNA se	6.54
	432639	AW973785		gb:EST385888 MAGE resequences, MAGM Homo	6.54
	410116	AW630871	Hs.58638	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CLLL7 protein	6.53
	442914	AW188551	Hs.98519	hypothetical protein FLJ14007	6.53
	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
75	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
80	436217	T53925	Hs.107	fibrinogen-like 1	6.46
	435809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB008284	Hs.51152	exostosins (multiple)-like 2	6.43
	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2266	secretory granule, neuroendocrine protol	6.40
	452198	AJ097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
5	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma fib	6.36
	451389	N73222	Hs.279009	matrix Gla protein	6.38
	427899	AA829286	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.226320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99540	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444856	AJ277924	Hs.145199	ESTs	6.30
15	433607	AA602004	Hs.23260	ESTs	6.26
	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AJ023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
20	447500	AJ361900	Hs.159212	ESTs	6.24
	407237	AA168872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	ACC03034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
25	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
	416857	AA188775	Hs.292453	ESTs	6.20
	427687	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
30	438940	AF075045	Hs.271609	ESTs	6.18
	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
35	427513	AJ476318	Hs.192480	ESTs	6.10
	448934	AJ598134	Hs.225592	ESTs, Highly similar to T61145 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239881	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
40	409048	H59990	Hs.37699	ESTs	6.08
	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33888	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	6.05
45	408243	Y00787	Hs.624	Interleukin 8	6.04
	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA983024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AJ928513	Hs.59203	ESTs	6.04
	428046	AW612795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.04
50	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.02
	442116	AJ884570	Hs.128813	ESTs	6.00
	423688	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
55	434739	AA804487	Hs.144130	ESTs	5.98
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.288	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.158054	ESTs	5.94
60	439096	AA830185	Hs.269680	ESTs	5.94
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (hs	5.94
	417246	AJ760088	Hs.21411	ESTs	5.94
	433190	M26801	Hs.3210	retin	5.92
65	418744	AJ887288	Hs.196378	ESTs, Weakly similar to putative p150 [H	5.92
	421477	AJ904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AJ791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
70	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
	408887	AA437199	Hs.656	cell division cycle 25C	5.90
	409843	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AJ863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
75	454853	AW812227		gb:RC2-STD173-201099-011-g09 ST0173 Homo	5.87
	457876	AJ821840	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455630	AV655701	Hs.76183	cytochrome P450, subfamily IIE (ethanol-	5.86
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
80	409045	AA635062	Hs.61084	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	5.84
	441845	AJ222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AJ538323	Hs.52620	Integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
5	439303	W00605	Hs.102784	ESTs	5.80
	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	438527	AW298119	Hs.202536	ESTs	5.78
10	435380	AA679001	Hs.192221	ESTs	5.78
	424086	AJ351010	Hs.102267	lysyl oxidase	5.76
	425898	AA365849	Hs.269478	ESTs, Weakly similar to PC4259 fertilin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	5.74
15	413982	BE503035	Hs.279193	ESTs	5.74
	453240	AJ968564	Hs.166254	hypothetical protein DKFZp566i133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AJ241331	Hs.131765	ESTs, Moderately similar to I38937 DNAR	5.72
20	448986	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
	433384	AJ021992	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
25	448565	NM_014953	Hs.323346	KIAA1008 protein	5.68
	412246	AJ160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AM78463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
30	422805	AA438989	Hs.121017	H2A histone family, member A	5.62
	442252	AJ733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	439040	AJ932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
35	433849	BE465884	Hs.280728	ESTs	5.58
	438639	AJ278360	Hs.31409	ESTs	5.58
	411274	NM_002778	Hs.89423	kalikrein 10	5.55
	435008	AF150262	Hs.162898	ESTs	5.55
	434184	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
40	452881	AW135220	Hs.241921	ESTs	5.54
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424482	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
45	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
	417543	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90316	KIAA0007 protein	5.51
	434874	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
50	418882	NM_004998	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AM69911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW185262		gb:mn67b05.x1 NCL_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.89233	zinc finger protein	5.46
	456435	AJ880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AJ198823	Hs.180473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
60	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452449	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187581	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	5.40
	441217	AJ922183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.40
	453691	AB037751	Hs.38353	Homo sapiens mRNA full length insert cDN	5.40
	408690	AW864542		gb:PM4-SN0016-120500-003-b02 SN0016 Homo	5.40
70	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	5.39
	446142	AJ754693	Hs.145968	ESTs	5.38
	408562	AI435323	Hs.31141	Homo sapiens mRNA for KIAA1558 protein,	5.36
	433929	AJ375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
75	424853	BE549737	Hs.132957	Human EST clone 122887 mariner transpos	5.34
	453931	AL121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.269423	ESTs	5.33
	416067	AJ927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
80	415091	AL044672	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
	445038	AJ635444	Hs.143917	dJ467NT1.1 protein	5.30
	408522	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA	NA	5.28
	449508	AK001566	Hs.23618 hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
5	414853	U31116	Hs.77501 sarcoglycan, beta (43kD dystrophin-assoc	5.28
	417372	T99755	Hs.334728 ESTs	5.28
	443613	AI079356	gb:cc39b09.s1 Soares_NhHMPu_S1 Homo sapi	5.28
	412610	X99908	Hs.74126 fatty acid binding protein 6, ileal (gas	5.27
	408943	NM_007070	Hs.49105 FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524 ESTs	5.26
	447982	H22953	Hs.137551 ESTs	5.26
	430789	AA632577	Hs.310235 ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AI824009	Hs.44577 ESTs	5.24
	409582	R27430	Hs.271565 ESTs	5.24
15	420911	U77413	Hs.100293 O-linked N-acetylglucosamine [GlcNAc] tr	5.23
	422956	BE545072	Hs.122579 hypothetical protein FLJ10461	5.23
	418661	NM_001949	Hs.1189 E2F transcription factor 3	5.22
	446271	D82484	Hs.330994 ESTs	5.22
	435905	AW997484	Hs.5003 KIAA0456 protein	5.21
20	434551	BE387162	Hs.280868 ESTs, Highly similar to A35661 DNA excis	5.21
	415245	N59660	Hs.27252 ESTs	5.20
	433016	AA808465	Hs.121536 Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278 KIAA1201 protein	5.20
	439818	AL360137	Hs.19934 Homo sapiens mRNA full length insert cDN	5.20
25	424281	AA766243	gb:cc13b11.s1 NC1_CGAP_GCB1 Homo sapiens	5.20
	449138	AW294215	Hs.195631 ESTs	5.20
	449416	AI651016	Hs.248311 ESTs	5.20
	430082	AI821389	Hs.16514 ESTs	5.20
	436574	AW293527	Hs.126465 ESTs	5.18
30	433377	AI752713	Hs.43845 ESTs	5.18
	440987	AA911705	Hs.130229 ESTs	5.18
	426116	AA868729	Hs.144694 ESTs	5.18
	441928	AI370188	Hs.211454 ESTs	5.17
	432657	AA831815	Hs.270840 ESTs, Weakly similar to I78885 serine/th	5.17
35	438011	BE466173	Hs.145696 splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.230931 ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722 interleukin 1, alpha	5.16
	433393	AF038584	Hs.98074 Itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810 ESTs	5.14
40	420170	U43374	Hs.95831 Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366 ESTs, Weakly similar to I78885 serine/th	5.12
	425739	T19016	Hs.159410 molybdopterin synthase sulfurylase	5.12
	440652	AI216751	Hs.143977 ESTs	5.12
	419706	C04649	Hs.77899 tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545 Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.118768 ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.118699 hypothetical protein FLJ12969	5.11
	407824	AW157431	Hs.246941 ESTs	5.11
	447197	R36075	gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.11
50	452465	AA810211	Hs.34244 ESTs	5.10
	442833	AA328153	Hs.88201 ESTs, Weakly similar to A Chain A, Cryst	5.10
	448852	AI609595	Hs.208038 ESTs	5.10
	408170	AW204516	Hs.31835 ESTs	5.08
	424238	AA337401	Hs.137635 ESTs	5.07
55	421072	AI216069	Hs.89113 ESTs	5.06
	424717	H03754	Hs.152213 wingless-type MMTV integration site fami	5.06
	423854	AI674253	Hs.35828 ESTs	5.06
	436862	AI821940	Hs.284622 ESTs, Moderately similar to ALU8_HUMAN A	5.06
	436554	AI985810	Hs.301173 ESTs	5.05
60	433284	DB5782	Hs.3229 cysteine dioxygenase, type I	5.04
	452387	AI880772	Hs.305094 trinucleotide repeat containing 12	5.04
	412656	AL080118	Hs.74420 origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759 ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	5.00
65	418217	AI910847	Hs.13442 ESTs	5.00
	401480	NA	NA	5.00
	456179	H75490	Hs.271930 ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
75	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	408690	107490_1	AW864542 AA056567 AW882724
	411765	125700_1	H43346 AA248302 AA095182
	414372	143909_1	AA143854 AW753140 AA213770 AW970865 AA589075 AA492132
80	424281	237742_1	AA766243 AA338252 AA338213

5	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488085
	432340	345248_1	AA534222 AA632632 TB1234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H80163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI079356 W23287
	447197	711623_1	R36076 AI366546 R36187
	447974	745643_1	R76886 AI453674 R77049
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543650_1	AF069478 AF089479 AF069480

TABLE 7C

20	Key:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

25	Key	Ref	Strand	Nt_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
30	401480	7321503	Plus	166120-166347,166451-166657,169651-169832
	401714	6715702	Plus	98484-98681
	401742	2911728	Plus	64003-64147
	403432	9719611	Minus	68204-68392
	403776	7770611	Minus	1414-1513,1624-1756
35	404227	7838233	Minus	93110-93259
	404567	7248169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38698,39727-39872,40557-40674,42351-42450
40	405360	9256107	Minus	7513-7573

Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

	Key:	Unique Eos probeset identifier number
	ExAcn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
50	Rt:	Ratio of tumor to normal colon

	Key	ExAcn	UnigeneID	Unigene Title	Rt
55	421996	AW583807	Hs.1460	glucagon	0.0233
	429970	AK000072	Hs.227069	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0416
	423690	AA328648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	0.0564
60	426851	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
	425920	AL049977	Hs.162209	claudin 8	0.0601
	431436	AA505035	Hs.195651	ESTs	0.0607
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
65	442009	AI733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.0707
	429050	X81333	Hs.194777	mesrin A, beta	0.0714
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
70	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429857	D13626	Hs.2465	KIAA0001 gene product; putative G-prote	0.0769
	443606	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypothet	0.0838
	415314	N88802	Hs.5422	glycoprotein M6B	0.0853
	451181	AI798330	Hs.207461	ESTs	0.0873
	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
	426835	BE395109	Hs.128327	hypothetical protein MGC13057	0.0900
	429350	AI754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

5	411529	AA430348	Hs.317598	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0967
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
	433546	AJ076877	Hs.125461	hypothetical protein FLJ11539	0.1007
	415154	D63175		gb:HUM501809B Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63587	Hs.2996	sucrase-isomaltase	0.1107
10	430468	NM_004673	Hs.241519	angiotensin-like 1	0.1114
	427167	AJ239507	Hs.99196	hypothetical protein MGC11324	0.1147
	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423606	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
15	412639	AW961284	Hs.296235	ESTs	0.1239
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
	403546				0.1248
	421913	AJ934365	Hs.109439	osteoglycin (osteoclast-inductive factor, mtrn	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
20	449835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
25	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.1328
	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm3003.x1 NCL_CGAP_Thy4 Homo sapiens	0.1393
	416586	X54162	Hs.79386	telomodin 1 (smooth muscle)	0.1395
30	436869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
	404767				0.1460
	407286	AJ235864		gb:Homo sapiens mRNA for immunoglobulin	0.1482
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1483
35	452768	AW069459	Hs.61539	ESTs	0.1486
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
	414881	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:Hsapiens mRNA for CD58 T3 protein.	0.1486
	402076				0.1487
40	453500	AA478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44585	ESTs	0.1500
	431706	AJ816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AJ824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84655	thin immunoglobulin domain protein (myo	0.1529
45	436056	AW023337	Hs.5422	glycoprotein M6B	0.1532
	428034	AJ278989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
	428609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
50	445200	AA084460	Hs.12409	somatostatin	0.1558
	443238	T78886	Hs.284450	ESTs	0.1563
	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
55	437734	AA653951	Hs.180284	ESTs	0.1637
	414290	AJ568801	Hs.71721	ESTs	0.1638
	418835	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AJ365585	Hs.146246	ESTs	0.1660
	442496	R55073	Hs.124130	ESTs	0.1676
60	450693	AW450461	Hs.203965	ESTs	0.1698
	420738	AJ263022	Hs.82204	ESTs	0.1718
	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176858	aquaporin 8	0.1757
65	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
	412056	T28160	Hs.778	guanylate cyclase activator 1B (refna)	0.1769
	406960	S69265		(NONE)	0.1781
	421666	AL035250	Hs.1408	endothelin 3	0.1784
70	452854	AA437061	Hs.14060	prokineticin 1 precursor	0.1795
	408514				0.1805
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AJ694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131468	Hs.23767	hypothetical protein FLJ12666	0.1812
75	412474	AF791451		gb:nt50c09.y5 NCL_CGAP_Ov2 Homo sapiens	0.1812
	436008	AJ078428	Hs.58785	ESTs	0.1820
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.265107	multimerin	0.1832
	419748	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
80	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AJ560944	Hs.71428	ESTs	0.1845

	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
10	436659	AI217900	Hs.144464	ESTs	0.1906
	447164	AF026941	Hs.17518	Homo sapiens cigs mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA426240	Hs.126083	ESTs	0.1942
15	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
	434683	AW298724	Hs.202639	ESTs	0.1957
	421885	AA609911	Hs.108012	MAX dimerization protein	0.1957
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypothet	0.1989
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
20	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
	437740	AA810265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	416961	BE391476	Hs.80617	ribosomal protein S16	0.2041
25	401455				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M236	0.2049
	416231	H30333	Hs.165052	ESTs	0.2049
	401753				0.2050
	433430	AI863735	Hs.186755	ESTs	0.2051
30	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.2058
	403957				0.2063
	436900	AI243036	Hs.18094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419566	AL137939	Hs.40096	ESTs	0.2090
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	428452	AW614271	Hs.121847	ESTs, Highly similar to AC006014 8 smil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI018777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
45	437354	AA749215	Hs.291886	ESTs	0.2137
	447734	AI421412	Hs.163659	ESTs	0.2144
	424685	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188099	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 cm	0.2151
50	401521				0.2157
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (0.2165
	401024				0.2171
	414802	AI793107	Hs.27018	Rts	0.2179
55	441083	BE562811		gb:801336446F1 NIH_MGC_44 Homo sapiens c	0.2185
	417355	D13168	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.212923	ESTs	0.2189
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypothet	0.2212
60	405654				0.2217
	415471	F09747	Hs.288707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA825499		gb:af65g08.r1 Soares_NihHMPu_S1 Homo sapi	0.2242
65	427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:801276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	458395	Z30300	Hs.281935	ESTs	0.2257
	439039	AI655707	Hs.48713	ESTs	0.2268
	433575	AA600175	Hs.39720	ESTs	0.2268
70	418095	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	AI372588	Hs.8022	TU3A protein	0.2283
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.2290
75	434839	AI743059	Hs.134736	ESTs	0.2294
	435731	AA699581	Hs.186811	ESTs	0.2299
	400865				0.2304
	446294	AI284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens	0.2305
80	414193	BE250069		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
	411514	AW850178		gb:IL3-CT0219-271099-D22-H12 CT0219 Homo	0.2315
	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.25556	tumor necrosis factor receptor superfam	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
	443482	AW188093	Hs.250385	ESTs	0.2326

5	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21365	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95296	ESTs	0.2347
	409331	M36634	Hs.53973	vasoactive intestinal peptide	0.2351
10	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99367	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
15	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18706	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
20	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279639	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
25	412622	AW864708	Hs.171969	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
	405073				0.2445
30	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
	426888	AW500131	Hs.171763	CD22 antigen	0.2471
35	427078	AI676062	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AA884208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
40	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2506
	408345	R93851	Hs.63053	ESTs	0.2506
	418353	L02640	Hs.84244	potassium voltage-gated channel, Shab-re	0.2508
45	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449383	R82252	Hs.108106	protein kinase (cAMP-dependent, catalytic)	0.2516
	459275	AI808813	Hs.393352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
	408897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
50	422743	BE304878	Hs.119598	ribosomal protein L3	0.2526
	458688	U72671	Hs.161250	intercellular adhesion molecule 5, telom	0.2532
	450880	AK002183	Hs.286885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F08972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
55	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
	453982	AW014995	Hs.281080	ESTs	0.2569
60	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE289427	Hs.21446	KIAA1716 protein	0.2579
	406134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	0.2580
	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
65	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.98857	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
70	437032	AW857372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628439	Hs.271296	ESTs, Weekly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1859	paraoxonase 1	0.2611
75	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450786	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
80	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

5	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	A1753134	Hs.146494	ESTs	0.2668
	416022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
	422909	AA533356		gb:n87110.s1 NCI_CGAP_Pr10 Homo sapiens	0.2681
10	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE538836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
	402425				0.2710
	460545	AW135582	Hs.201767	ESTs	0.2710
15	417118	U38854	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	FD6844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
	441493	AW070446	Hs.127037	ESTs	0.2733
	413541	BE147038		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
20	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone C3T	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cys	0.2740
	444195	AB002361	Hs.10587	KIAA0353 protein	0.2743
	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen	0.2747
25	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063821	Hs.295971	ESTs	0.2755
	414378	BE393856	Hs.06915	ESTs, Weakly similar to 16.7Kd protein [0.2756
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
	432018	AA524447	Hs.152377	ESTs	0.2763
30	422854	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	416397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	AI024834	Hs.131729	ESTs	0.2775
	410850	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
	427114	AI218896	Hs.97592	ESTs	0.2778
35	448466	AI522109	Hs.171066	ESTs	0.2778
	434445	AI349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:n63c07.s1 NCI_CGAP_Pr1 Homo sapiens	0.2785
	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	0.2786
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
40	433633	AI880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	406691				0.2804
	406334				0.2804
	403047				0.2809
45	412506	AW957158		gb:EST369229 MAGI2 resequences, MAGD Homo	0.2809
	441042	AA077736		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
	444453	AW378394	Hs.145126	ESTs	0.2817
	457736	AK000390	Hs.4205	hypothetical protein FLJ20124	0.2820
50	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08988	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
	435021	AA922192	Hs.54709	ESTs	0.2828
	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
55	447787	BE620108		gb:801483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	458244	AI929453	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	0.2841
	437463	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
	407898	AA905097	Hs.85050	phospholamban	0.2845
60	417332	AW972717	Hs.289462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	HO4607	Hs.0218	ESTs	0.2857
	425195	AA352026	Hs.94319	VP510 domain receptor protein	0.2857
	404769				0.2863
65	411620	AW854536		gb:RC3-CT0255-200100-024-a08 CT0255 Homo	0.2868
	426746	AW503820	Hs.192861	Sp1-8 transcription factor (Sp1-1/PU.1 r	0.2870
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	0.2872
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
	422033	AW245806	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
70	421935	AA131632	Hs.109672	CMP-NeuAc(beta)-N-acetylglucosaminide	0.2878
	447955	BE544271	Hs.288360	hypothetical protein FLJ22795	0.2880
	406354				0.2881
	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
	431087	H12723	Hs.290791	ESTs	0.2882
75	450610	AA018370	Hs.60386	nuclear RNA export factor 3	0.2882
	446827	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148387	ESTs	0.2886
	445152	AI214667	Hs.283597	ESTs	0.2891
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
80	455614	AI693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA765694	Hs.123298	ESTs	0.2913
	444459	AI680624	Hs.148876	ESTs	0.2913
	444918	AI202262	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

5	413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
	443998	AI620661	Hs.296276	ESTs	0.2924
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
	421204	AW081587	Hs.165061	ESTs	0.2928
	420831	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
10	440507	H06894		gb:U81b07.r1 Soares infant brain 1N1B H	0.2943
	445555	AW974013	Hs.260809	ESTs	0.2945
	438570	AW888554	Hs.84296	CD74 antigen (invariant polypeptide of m	0.2948
	447195	T73745	Hs.279670	ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
15	421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
	433745	AF075320	Hs.289980	hypothetical protein FLJ14540	0.2969
	417935	R53697	Hs.170044	ESTs	0.2970
20	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
	413537	BE146866		gb:QV4-HT0222-211099-014-R05 HT0222 Homo	0.2973
	445194	AI215687	Hs.175044	ESTs	0.2974
	454135	AW139965	Hs.246783	ESTs	0.2976
	403418				0.2986
25	457805	AV857778	Hs.3314	selenoprotein P, plasma, 1	0.2989
	408896	AI610447	Hs.48778	ribon protein	0.2993
	448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
	417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637	Hs.173739	hypothetical protein FLJ10287	0.2996
30	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.3000
	451531	AA018311	Hs.114762	ESTs	0.3003
	444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407368	AF026942		gb:Homo sapiens c1g33 mRNA, partial sequ	0.3012
35	459456	AA486036	Hs.190124	ESTs	0.3012
	417111	AW016321	Hs.82306	desitin (actin depolymerizing factor)	0.3012
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
	410482	AW772187	Hs.191859	ESTs	0.3013
40	417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
	404414				0.3019
	432247	AA531287	Hs.105805	ESTs	0.3023
	453471	AL037887	Hs.208179	ESTs	0.3025
	417481	AA203281	Hs.21798	ESTs	0.3029
45	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
	448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
	429223	BE264152	Hs.221994	ESTs	0.3034
	404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
	406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
50	438839	AW297945	Hs.128490	ESTs	0.3039
	431848	AI378857	Hs.128758	ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3046
	458789	AL157468	Hs.325625	Homo sapiens cDNA FLJ20848 fis, clone AD	0.3048
	443294	AI733625	Hs.133053	ESTs	0.3050
55	447023	AA356764	Hs.17109	Integral membrane protein 2A	0.3052
	458583	AI479646	Hs.157081	hypothetical protein MGC4170	0.3056
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	0.3067
	445123	AI762911	Hs.145369	ESTs	0.3068
	412882	AW983772		gb:RC3-HN0002-660400-012-h09 HN0002 Homo	0.3066
60	434361	AF129755	Hs.117772	ESTs	0.3071
	414026	BE241713		gb:TCAP1E0472 Pediatric acute myelogeno	0.3072
	432149	AW814326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
	408350	AW183950	Hs.250127	ESTs	0.3074
	401042				0.3077
65	422588	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
	438692	AB007850	Hs.6360	KIAA0481 gene product	0.3077
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3669590, mRNA,	0.3083
	444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	0.3088
70	430410	AF089144	Hs.250700	tryptase beta 1	0.3090
	419298	AI311085	Hs.82406	hypothetical protein FLJ22573	0.3091
	400672				0.3094
	444010	AW976457	Hs.282887	ESTs	0.3096
	451699	AL118571	Hs.121657	ESTs, Weakly similar to DPL_HUMAN POLYPO	0.3096
75	432471	BE244667	Hs.296155	CGI-100 protein	0.3105
	405277				0.3106
	456765	AI487900	Hs.33057	ESTs	0.3108
	452090	AA022684	Hs.124573	Homo sapiens cDNA FLJ11477 fis, clone HE	0.3106
	426497	AA379913		gb:EST92807 Skin tumor 1 Homo sapiens cD	0.3106
80	406582				0.3106
	423521	BE002904		gb:QV4-BN0090-070400-163-e07 BN0090 Homo	0.3107
	417919	AI928203	Hs.86379	ESTs	0.3110
	414484	BE314385		gb:801154649F1 NIH_MGC_19 Homo sapiens c	0.3110
	457439	AW410408	Hs.271167	L-plasmaic acid oxidase	0.3116
	426449	AI134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
	458544	AI631036	Hs.196843	ESTs	0.3119

5	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypothet	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170691	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
	451385	AA017656		gb:z39h01.r1 Scars retina N2b4HR Homo	0.3125
	446404	AA019961	Hs.26216	LOC50627	0.3130
10	446516	R65964	Hs.241569	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.128056	ESTs	0.3136
	417318	AW953937	Hs.12691	ESTs	0.3139
	443980	AI459140	Hs.299087	ESTs	0.3140
	459138	AI903291		gb:RC-BT029-080199-047 BT029 Homo saplen	0.3142
15	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135276	Hs.192311	ESTs	0.3143
	414214	D49958	Hs.75819	glycoprotein M6A	0.3145
	446378	AI905699	Hs.239769	citrate synthase	0.3145
	459233	AI939966		gb:MR0-CT0015-160799-002-b08 CT0015 Homo	0.3146
20	428193	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.231444	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.145601	ESTs	0.3153
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
	405071				0.3160
25	407457	AJ242724		gb:Homo sapiens mRNA for partial putativ	0.3162
	408922	AW505582	Hs.130732	KIAA1575 protein	0.3172
	438219	AI916151	Hs.257194	ESTs	0.3173
	412944	AA384110	Hs.197143	ESTs	0.3175
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.3178
30	426662	AA879474	Hs.122710	ESTs	0.3178
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	0.3179
	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	0.3181
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	0.3183
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	0.3185
35	448812	H30776	Hs.22140	BM88 antigen	0.3188
	411288	AW835511		gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
	422884	AW860976	Hs.13256	ESTs	0.3190
	405535				0.3195
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting enkyrin-rela	0.3195
40	455353	W26786		gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.306669	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428568	AC004755	Hs.184922	Homo sapiens chromosome 19, fosmid 37502	0.3195
	429106	BE620016	Hs.182470	PTD010 protein	0.3198
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
45	445682	AW378397		gb:RC3-HT0220-031299-012-g06 HT0220 Homo	0.3205
	437568	AI954795	Hs.156135	ESTs	0.3205
	448943	AI808810	Hs.193288	ESTs	0.3205
	431998	AI133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207
	419278	AA235800	Hs.87500	ESTs	0.3208
50	405913				0.3209
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.3212
	424729	AF063012	Hs.152531	heart and neural crest derivatives expro	0.3212
	440020	AI480204	Hs.177131	ESTs	0.3213
	429082	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	0.3215
55	433683	AF083131	Hs.228635	CATX-15 protein	0.3215
	400641				0.3216
	408140				0.3216
	415280	R59473	Hs.268715	ESTs	0.3217
	447635	AI869669	Hs.195362	ESTs	0.3217
60	401887				0.3217
	400787				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
	448758	AB018311	Hs.21817	KIAA0768 protein	0.3222
	444750	AW242684	Hs.243823	ESTs	0.3223
65	411466	AW847669		gb:IL3-CT0213-280100-058-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.278909	Interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
	433234	AB040928	Hs.65366	KIAA1495 protein	0.3231
	422831	R02504	Hs.332943	ESTs	0.3234
70	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypothet	0.3236
	446901	AI347274		gb:td05d02x1 NCL CGAP_Co16 Homo sapiens	0.3242
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
	445848	AA774824	Hs.13377	Homo sapiens clone Z3649 and Z3755 unifo	0.3257
75	441143	AI027604	Hs.159650	ESTs	0.3257
	405138				0.3262
	412888	M88151		gb:EST02679 Hippocampus, Stralagena (cat	0.3262
	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.270840	ESTs	0.3263
80	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.305752	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
	431851	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3267
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768853	Hs.134478	ESTs	0.3269
	451095	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

	454947	AW846590	gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275	
	413814	BE159592	gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275	
5	422818	AA404290	Hs.97848	ESTs	0.3277
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.3278
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	0.3278
	452164	AI853171	gb:tz44b02.x1 NCI_CGAP_Bm52 Homo sapien	0.3279	
	458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated	0.3279
	433197	AB040889	Hs.281022	KIAA1456 protein	0.3280
	405701				0.3282
10	437782	AI370876	Hs.79090	exportin 1 (CRM1, yeast, homolog)	0.3284
	459001	AI761313	Hs.204606	ESTs	0.3286
	422783	AA598956	Hs.120439	ethanolamine kinase	0.3289
	417036	AF039918	Hs.80975	ectonucleoside triphosphate diphosphohyd	0.3290
	456041	BE270795	Hs.268864	ESTs	0.3295
15	423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296
	427530	AA405093	Hs.126519	ESTs	0.3296
	420172	AA601122	Hs.95655	secreted and transmembrane 1	0.3297
	445610	AI831648	Hs.143993	ESTs	0.3297
20	411328	AW837083	gb:QV1-LT0037-150200-089-g08 LT0037 Homo	0.3300	

Table BB

25	Pkey:	Unique Ecos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

Pkey	CAT number	Accession
30	409921	1159516_1 AW600239 AW500255 AW505332
	410626	1212621_1 BE407727
	410845	1223881_1 AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807266 AW807097 AW807270 AW807372 AW807260 AW807283
	410950	1227728_1 AW811633 AW811652 AW811898
35	411288	1237709_1 AW835511 AW835517 AW835513
	411319	1238595_1 BE537094 AW836542
	411328	1238987_1 AW837063 AW935882 AW935957
	411466	1248771_1 AW847669 AW847667 BE145799
	411514	1248638_1 AW850178 AW850233 AW850445 AW850448
40	411620	1252014_1 AW854536 AW854417 AW854495 AW854355
	411880	1263110_1 AW872477 BE088101 T05390
	412474	128869_1 AI791451 AI791288 BE019234 BE296601 AA111939
	412506	1301336_1 AW957159 H09937 T75143
	412682	1321572_1 AW983772 AW983730 AW983769 AW983836 AW983835 AW983837
45	412888	1334784_1 M85151 BE061884 BE061893 BE061898 BE061882 BE061887 BE061891 BE061890 BE061895 BE061894 BE061886 BE061885 BE061886 BE061887 BE061888 BE061889 BE061890 BE061891 BE061892 BE061893 BE061894 BE061895 BE061896 BE061897 BE061898 BE061899 BE061900 BE061901 BE061902 BE061903 BE061904 BE061905 BE061906 BE061907 BE061908 BE061909 BE061910 BE061911 BE061912 BE061913 BE061914 BE061915 BE061916 BE061917 BE061918 BE061919 BE061920 BE061921 BE061922 BE061923 BE061924 BE061925 BE061926 BE061927 BE061928 BE061929 BE061930 BE061931 BE061932 BE061933 BE061934 BE061935 BE061936 BE061937 BE061938 BE061939 BE061940 BE061941 BE061942 BE061943 BE061944 BE061945 BE061946 BE061947 BE061948 BE061949 BE061950 BE061951 BE061952 BE061953 BE061954 BE061955 BE061956 BE061957 BE061958 BE061959 BE061960 BE061961 BE061962 BE061963 BE061964 BE061965 BE061966 BE061967 BE061968 BE061969 BE061970 BE061971 BE061972 BE061973 BE061974 BE061975 BE061976 BE061977 BE061978 BE061979 BE061980 BE061981 BE061982 BE061983 BE061984 BE061985 BE061986 BE061987 BE061988 BE061989 BE061990 BE061991 BE061992 BE061993 BE061994 BE061995 BE061996 BE061997 BE061998 BE061999 BE062000 BE062001 BE062002 BE062003 BE062004 BE062005 BE062006 BE062007 BE062008 BE062009 BE062010 BE062011 BE062012 BE062013 BE062014 BE062015 BE062016 BE062017 BE062018 BE062019 BE062020 BE062021 BE062022 BE062023 BE062024 BE062025 BE062026 BE062027 BE062028 BE062029 BE062030 BE062031 BE062032 BE062033 BE062034 BE062035 BE062036 BE062037 BE062038 BE062039 BE062040 BE062041 BE062042 BE062043 BE062044 BE062045 BE062046 BE062047 BE062048 BE062049 BE062050 BE062051 BE062052 BE062053 BE062054 BE062055 BE062056 BE062057 BE062058 BE062059 BE062060 BE062061 BE062062 BE062063 BE062064 BE062065 BE062066 BE062067 BE062068 BE062069 BE062070 BE062071 BE062072 BE062073 BE062074 BE062075 BE062076 BE062077 BE062078 BE062079 BE062080 BE062081 BE062082 BE062083 BE062084 BE062085 BE062086 BE062087 BE062088 BE062089 BE062090 BE062091 BE062092 BE062093 BE062094 BE062095 BE062096 BE062097 BE062098 BE062099 BE062100 BE062101 BE062102 BE062103 BE062104 BE062105 BE062106 BE062107 BE062108 BE062109 BE062110 BE062111 BE062112 BE062113 BE062114 BE062115 BE062116 BE062117 BE062118 BE062119 BE062120 BE062121 BE062122 BE062123 BE062124 BE062125 BE062126 BE062127 BE062128 BE062129 BE062130 BE062131 BE062132 BE062133 BE062134 BE062135 BE062136 BE062137 BE062138 BE062139 BE062140 BE062141 BE062142 BE062143 BE062144 BE062145 BE062146 BE062147 BE062148 BE062149 BE062150 BE062151 BE062152 BE062153 BE062154 BE062155 BE062156 BE062157 BE062158 BE062159 BE062160 BE062161 BE062162 BE062163 BE062164 BE062165 BE062166 BE062167 BE062168 BE062169 BE062170 BE062171 BE062172 BE062173 BE062174 BE062175 BE062176 BE062177 BE062178 BE062179 BE062180 BE062181 BE062182 BE062183 BE062184 BE062185 BE062186 BE062187 BE062188 BE062189 BE062190 BE062191 BE062192 BE062193 BE062194 BE062195 BE062196 BE062197 BE062198 BE062199 BE062200 BE062201 BE062202 BE062203 BE062204 BE062205 BE062206 BE062207 BE062208 BE062209 BE062210 BE062211 BE062212 BE062213 BE062214 BE062215 BE062216 BE062217 BE062218 BE062219 BE062220 BE062221 BE062222 BE062223 BE062224 BE062225 BE062226 BE062227 BE062228 BE062229 BE062230 BE062231 BE062232 BE062233 BE062234 BE062235 BE062236 BE062237 BE062238 BE062239 BE062240 BE062241 BE062242 BE062243 BE062244 BE062245 BE062246 BE062247 BE062248 BE062249 BE062250 BE062251 BE062252 BE062253 BE062254 BE062255 BE062256 BE062257 BE062258 BE062259 BE062260 BE062261 BE062262 BE062263 BE062264 BE062265 BE062266 BE062267 BE062268 BE062269 BE062270 BE062271 BE062272 BE062273 BE062274 BE062275 BE062276 BE062277 BE062278 BE062279 BE062280 BE062281 BE062282 BE062283 BE062284 BE062285 BE062286 BE062287 BE062288 BE062289 BE062290 BE062291 BE062292 BE062293 BE062294 BE062295 BE062296 BE062297 BE062298 BE062299 BE062300 BE062301 BE062302 BE062303 BE062304 BE062305 BE062306 BE062307 BE062308 BE062309 BE062310 BE062311 BE062312 BE062313 BE062314 BE062315 BE062316 BE062317 BE062318 BE062319 BE062320 BE062321 BE062322 BE062323 BE062324 BE062325 BE062326 BE062327 BE062328 BE062329 BE062330 BE062331 BE062332 BE062333 BE062334 BE062335 BE062336 BE062337 BE062338 BE062339 BE062340 BE062341 BE062342 BE062343 BE062344 BE062345 BE062346 BE062347 BE062348 BE062349 BE062350 BE062351 BE062352 BE062353 BE062354 BE062355 BE062356 BE062357 BE062358 BE062359 BE062360 BE062361 BE062362 BE062363 BE062364 BE062365 BE062366 BE062367 BE062368 BE062369 BE062370 BE062371 BE062372 BE062373 BE062374 BE062375 BE062376 BE062377 BE062378 BE062379 BE062380 BE062381 BE062382 BE062383 BE062384 BE062385 BE062386 BE062387 BE062388 BE062389 BE062390 BE062391 BE062392 BE062393 BE062394 BE062395 BE062396 BE062397 BE062398 BE062399 BE062400 BE062401 BE062402 BE062403 BE062404 BE062405 BE062406 BE062407 BE062408 BE062409 BE062410 BE062411 BE062412 BE062413 BE062414 BE062415 BE062416 BE062417 BE062418 BE062419 BE062420 BE062421 BE062422 BE062423 BE062424 BE062425 BE062426 BE062427 BE062428 BE062429 BE062430 BE062431 BE062432 BE062433 BE062434 BE062435 BE062436 BE062437 BE062438 BE062439 BE062440 BE062441 BE062442 BE062443 BE062444 BE062445 BE062446 BE062447 BE062448 BE062449 BE062450 BE062451 BE062452 BE062453 BE062454 BE062455 BE062456 BE062457 BE062458 BE062459 BE062460 BE062461 BE062462 BE062463 BE062464 BE062465 BE062466 BE062467 BE062468 BE062469 BE062470 BE062471 BE062472 BE062473 BE062474 BE062475 BE062476 BE062477 BE062478 BE062479 BE062480 BE062481 BE062482 BE062483 BE062484 BE062485 BE062486 BE062487 BE062488 BE062489 BE062490 BE062491 BE062492 BE062493 BE062494 BE062495 BE062496 BE062497 BE062498 BE062499 BE062500 BE062501 BE062502 BE062503 BE062504 BE062505 BE062506 BE062507 BE062508 BE062509 BE062510 BE062511 BE062512 BE062513 BE062514 BE062515 BE062516 BE062517 BE062518 BE062519 BE062520 BE062521 BE062522 BE062523 BE062524 BE062525 BE062526 BE062527 BE062528 BE062529 BE062530 BE062531 BE062532 BE062533 BE062534 BE062535 BE062536 BE062537 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BE062760 BE062761 BE062762 BE062763 BE062764 BE062765 BE062766 BE062767 BE062768 BE062769 BE062770 BE062771 BE062772 BE062773 BE062774 BE062775 BE062776 BE062777 BE062778 BE062779 BE062780 BE062781 BE062782 BE062783 BE062784 BE062785 BE062786 BE062787 BE062788 BE062789 BE062790 BE062791 BE062792 BE062793 BE062794 BE062795 BE062796 BE062797 BE062798 BE062799 BE062800 BE062801 BE062802 BE062803 BE062804 BE062805 BE062806 BE062807 BE062808 BE062809 BE062810 BE062811 BE062812 BE062813 BE062814 BE062815 BE062816 BE062817 BE062818 BE062819 BE062820 BE062821 BE062822 BE062823 BE062824 BE062825 BE062826 BE062827 BE062828 BE062829 BE062830 BE062831 BE062832 BE062833 BE062834 BE062835 BE062836 BE062837 BE062838 BE062839 BE062840 BE062841 BE062842 BE062843 BE062844 BE062845 BE062846 BE062847 BE062848 BE062849 BE062850 BE062851 BE062852 BE062853 BE062854 BE062855 BE062856 BE062857 BE062858 BE062859 BE062860 BE062861 BE062862 BE062863 BE062864 BE062865 BE062866 BE062867 BE062868 BE062869 BE062870 BE062871 BE062872 BE062873 BE062874 BE062875 BE062876 BE062877 BE062878 BE062879 BE062880 BE062881 BE062882 BE062883 BE062884 BE062885 BE062886 BE062887 BE062888 BE062889 BE062890 BE062891 BE062892 BE062893 BE062894 BE062895 BE062896 BE062897 BE062898 BE062899 BE062900 BE062901 BE062902 BE062903 BE062904 BE062905 BE062906 BE062907 BE062908 BE062909 BE062910 BE062911 BE062912 BE062913 BE062914 BE062915 BE062916 BE062917 BE062918 BE062919 BE062920 BE062921 BE062922 BE062923 BE062924 BE062925 BE062926 BE062927 BE062928 BE062929 BE062930 BE062931 BE062932 BE062933 BE062934 BE062935 BE062936 BE062937 BE062938 BE062939 BE062940 BE062941 BE062942 BE062943 BE062944 BE062945 BE062946 BE062947 BE062948 BE062949 BE062950 BE062951 BE062952 BE062953 BE062954 BE062955 BE062956 BE062957 BE062958 BE062959 BE062960 BE062961 BE062962 BE062963 BE062964 BE062965 BE062966 BE062967 BE062968 BE062969 BE062970 BE062971 BE062972 BE062973 BE062974 BE062975 BE062976 BE062977 BE062978 BE062979 BE062980 BE062981 BE062982 BE062983 BE062984 BE062985 BE062986 BE062987 BE062988 BE062989 BE062990 BE062991 BE062992 BE062993 BE062994 BE062995 BE062996 BE062997 BE062998 BE062999 BE063000 BE063001 BE063002 BE063003 BE063004 BE063005 BE063006 BE063007 BE063008 BE063009 BE063010 BE063011 BE063012 BE063013 BE063014 BE063015 BE063016 BE063017 BE063018 BE063019 BE063020 BE063021 BE063022 BE063023 BE063024 BE063025 BE063026 BE063027 BE063028 BE063029 BE063030 BE063031 BE063032 BE063033 BE063034 BE063035 BE063036 BE063037 BE063038 BE063039 BE063040 BE063041 BE063042 BE063043 BE063044 BE063045 BE063046 BE063047 BE063048 BE063049 BE063050 BE063051 BE063052 BE063053 BE063054 BE063055 BE063056 BE063057 BE063058 BE063059 BE063060 BE063061 BE063062 BE063063 BE063064 BE063065 BE063066 BE063067 BE063068 BE063069 BE063070 BE063071 BE063072 BE063073 BE063074 BE063075 BE063076 BE063077 BE063078 BE063079 BE063080 BE063081 BE063082 BE063083 BE063084 BE063085 BE063086 BE063087 BE063088 BE063089 BE063090 BE063091 BE063092 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BE063204 BE063205 BE063206 BE063207 BE063208 BE063209 BE063210 BE063211 BE063212 BE063213 BE063214 BE063215 BE063216 BE063217 BE063218 BE063219 BE063220 BE063221 BE063222 BE063223 BE063224 BE063225 BE063226 BE063227 BE063228 BE063229 BE063230 BE063231 BE063232 BE063233 BE063234 BE063235 BE063236 BE063237 BE063238 BE063239 BE063240 BE063241 BE063242 BE063243 BE063244 BE063245 BE063246 BE063247 BE063248 BE063249 BE063250 BE063251 BE063252 BE063253 BE063254 BE063255 BE063256 BE063257 BE063258 BE063259 BE063260 BE063261 BE063262 BE063263 BE063264 BE063265 BE063266 BE063267 BE063268 BE063269 BE063270 BE063271 BE063272 BE063273 BE063274 BE063

454790 1234752_1 AW820852 AW820773 AW821088
 454947 1245953_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
 455353 1284289_1 W26786 AW998612 AW902272
 457115 288601_1 AA420712 AA469165 AA420737
 459138 918860_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346
 459233 944881_1 AI939968 AI939968 AI939951 AI939981 AI939976 AI939959

Table 8C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400641	8117693	Plus	4786-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400865	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9650602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119557
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401763	9838183	Minus	155287-155529,159719-159997
401776	9968323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402610	9926549	Minus	22955-23124
402695	8568671	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404248	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	9212565	Plus	125032-125291
404638	9795751	Minus	99433-99528,100035-100161
404696	9800108	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8098713	Minus	175801-176823
404927	7342002	Plus	68680-69563
404958	7407941	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8578241	Plus	50303-50516
405277	3980473	Plus	23471-23572
405282	3810673	Minus	10482-10689
405334	3135285	Plus	139386-139856
405364	2281075	Minus	48325-48491,49135-49252
405385	6552772	Plus	48332-48454
405635	9795658	Plus	63384-63545
405610	6757553	Minus	71907-72080
405654	4895155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	5758747	Minus	55673-56287
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemptar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of tumor samples divided by the 70th percentile of normal body tissue samples, where the 15th percentile of normal body tissues was subtracted from the numerator and denominator

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
15	436749	AAS84890	Hs.5302	NM_006149: Homo sapiens lectin, galactosi	29.34
	406690	M29540	Hs.220629	(locuslink)NM_004363: Homo sapiens carc	25.56
	406667	M12523			20.28
	414386	X00442	Hs.76990	NM_005143: Homo sapiens haptoglobin (HP)	18.84
20	428934	AF039401	Hs.194659	NM_001285: Homo sapiens chloride channel,	17.38
	416768	AA363733	Hs.1032	NM_006507: Homo sapiens regenerating isle	18.99
	446787	U67167	Hs.315	NM_002457: Homo sapiens mucin 2, intestin	16.61
	431912	AI660552	Hs.356183	Hs.356183: ESTs, Weakly similar to S3B4_H	16.42
	437935	AW939591	Hs.5940	NM_033049: Homo sapiens mucin 13, epithel	15.92
	407242	M18728		(locuslink)NM_002483: Homo sapiens carc	15.84
25	423541	AA296822	Hs.129778	NM_014471: Homo sapiens serine protease I	15.59
	441031	AI110684	Hs.7645	NM_005141: Homo sapiens fibrinogen, B bet	15.02
	406685	M18728		(locuslink)NM_002483: Homo sapiens carc	14.54
	422578	AF239666	Hs.1545	NM_001804: Homo sapiens caudal type homeo	13.68
30	432542	AW083920	Hs.16098	NM_020384: Homo sapiens claudin 2 (CLDN2)	13.23
	421341	AJ243212	Hs.374281	NM_007329: Homo sapiens deleted in malign	13.21
	453963	X02544	Hs.572	Hs.572: orosomucoid 1	13.06
	421582	A1910275	Hs.350470	NM_003225: Homo sapiens trefol factor 1	12.35
	436217	T53925	Hs.107	NM_004467: Homo sapiens fibrinogen-like 1	12.11
	422260	AA315993	Hs.105484	NM_032044: Homo sapiens regenerating gene	11.99
35	418888	AJ076801	Hs.88436	NM_004063: Homo sapiens cadherin 17, Li c	11.87
	407243	AA068357	Hs.74466	(locuslink)NM_006890: Homo sapiens carc	11.81
	424212	NM_005814	Hs.143131	NM_005814: Homo sapiens glycoprotein A33	11.27
	414463	T69078	Hs.78177	NM_001633: Homo sapiens alpha-1-microglob	11.18
40	407007	U22961	Hs.184411	NM_000477: Homo sapiens albumin (ALB), mR	10.82
	413719	BE439560	Hs.75498	NM_004591: Homo sapiens small inducible c	10.73
	450685	L15533	Hs.423	NM_138938: Homo sapiens pancreatitis-asso	10.57
	418007	M13509	Hs.83169	NM_002421: Homo sapiens matrix metallopro	10.39
	423573	BE003054	Hs.1695	NM_002426: Homo sapiens matrix metallopro	10.10
	423371	AJ076819	Hs.1650	NM_000111: Homo sapiens solute carrier fa	9.91
45	421964	X73079	Hs.288579	NM_002644: Homo sapiens polymorphic immunog	9.68
	447400	AK000322	Hs.18457	NM_017763: Homo sapiens hypothetical prot	9.44
	421100	AW351639	Hs.124680	Hs.124680: ESTs, Moderately similar to 21	9.38
	406741	AA058357	Hs.74466	(locuslink)NM_006890: Homo sapiens carc	9.34
50	427583	M62962	Hs.179704	NM_005588: Homo sapiens maprin A, alpha (9.18
	422281	M36803	Hs.346935	NM_000613: Homo sapiens hemopexin (HPX),	9.06
	406687	M31126	Hs.352054	Hs.352054: pregnancy specific beta-1-glyc	9.02
	409153	W03754	Hs.50813	NM_017625: Homo sapiens intelectin (ITLN)	8.89
	424687	J05070	Hs.151738	NM_004994: Homo sapiens matrix metallopro	8.53
55	422664	AA315933	Hs.120879	Hs.120879: Homo sapiens, clone MGC:32871	8.23
	452304	AA025386	Hs.61311	Hs.61311: ESTs, Weakly similar to S10590	8.10
	430569	AF241254	Hs.178098	NM_021804: Homo sapiens angiotensin I con	8.05
	413861	L00190	Hs.75599	(locuslink)NM_000488: Homo sapiens serine	7.96
	406399				7.73
60	422424	AI186431	Hs.296638	Hs.296638: prostate differentiation facto	7.71
	428470	AC002301	Hs.184507	Hs.184507: Homo sapiens, similar to Homol	7.43
	417831	W95842	Hs.82961	Hs.82961: Homo sapiens, clone MGC:22588 1	7.40
	435538	AB011540	Hs.4930	Hs.4930: low density lipoprotein receptor	7.29
	430272	X04898	Hs.237858	Hs.237858: apolipoprotein A-II	7.25
65	451917	AW391351	Hs.60820	Hs.60820: hypothetical cardiac/skeletal m	7.21
	421907	BE018556	Hs.109358	Hs.109358: ATPase, Class V, type 10B	7.19
	452316	AA298484	Hs.61265	NM_139805: Homo sapiens family with sequo	7.18
	452594	AU076405	Hs.29981	Hs.29981: solute carrier family 25 (sulfa	7.03
	424328	NM_014479	Hs.145296	NM_014479: Homo sapiens ADAM-like, decysl	7.00
	443428	AF098168	Hs.9329	(locuslink)NM_012112: Homo sapiens chromo	6.92
70	452194	AI694413	Hs.373599	Hs.373599: EST	6.88
	411975	AI918056	Hs.144583	Hs.144583: Homo sapiens, clone IMAGE:3462	6.76
	408243	Y00787	Hs.624	NM_000584: Homo sapiens interleukin 8 (IL	6.59
	422310	AA316622	Hs.98370	(locuslink)NM_030622: Homo sapiens cytoch	6.55
75	431330	X69532	Hs.2777	NM_002215: Homo sapiens inter-alpha (glob	6.53
	420344	BE463721	Hs.97101	NM_014373: Homo sapiens putative G protai	6.49
	422330	D30783	Hs.115283	NM_001432: Homo sapiens ephregulin (EREG)	6.33
	412104	AW205197	Hs.240951	(locuslink)NM_033120: Homo sapiens naked	6.31
	461035	AU076785	Hs.430	NM_002670: Homo sapiens plastin 1 (Iscf	6.30
80	428753	AW938252	Hs.192927	NM_017726: Homo sapiens protein phosphata	6.29
	430577	Z26317	Hs.359784	NM_001943: Homo sapiens desmoglein 2 (DSG	6.28
	422487	AJ010901	Hs.198267	NM_018406: Homo sapiens mucin 4, tracheob	6.27
	444361	BE387335	Hs.283713	NM_138465: Homo sapiens collagen triple h	6.26
	409532	W74001	Hs.55279	NM_002639: Homo sapiens serine (or cystei	6.23

5	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23
	413936	AF113576	Hs.297681	NM_000295:Homo sapiens serine (or cystei	6.23
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	6.17
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	6.17
	415214	AJ445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.17
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.16
	422105	DB4239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	6.14
10	423803	NM_005709	Hs.132945	(locustink)NM_005709:Homo sapiens PIZ-73	6.13
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fls,	6.09
	447342	AJ199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	6.02
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	5.96
	403220				5.90
15	408908	BE296227	Hs.250822	(locustink)NM_003158:Homo sapiens serine	5.88
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	5.87
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	5.79
	414617	AJ339520	Hs.288817	(locustink)NM_025130:Homo sapiens hypoth	5.79
	408863	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis 1	5.77
20	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	431301	AA502384	Hs.151529	Hs.151529:ESTs	5.71
	416318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	5.71
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	5.68
25	436972	AA284679	Hs.25640	Hs.25640:claudin 3	5.66
	414987	AA524394	Hs.294022	NM_032855:Homo sapiens hypothetical prot	5.61
	431657	AJ345227	Hs.105448	Hs.105448:protein kinase, lysine deficite	5.67
	424273	W40460	Hs.144442	NM_003581:Homo sapiens phospholipase A2,	5.55
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.54
30	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.50
	426227	U67058	Hs.154299	(locustink)NM_005242:Homo sapiens coagut	5.38
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	5.33
	414809	AJ434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	5.32
35	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.32
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	5.28
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.28
	444151	AW872917	Hs.128749	(locustink)NM_014324:Homo sapiens alpha-	5.27
	438746	AJ885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.26
40	408704	AA066635	Hs.5388	NM_139053:Homo sapiens epidermal growth	5.25
	414786	AJ286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	5.25
	436251	BE515065	Hs.296585	(locustink)NM_005392:Homo sapiens nucleo	5.25
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.23
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	5.22
45	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interna	5.20
	432978	AF126743	Hs.279884	NM_013236:Homo sapiens DNAJ domain-conta	5.18
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.13
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	5.12
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	5.11
50	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.08
	426174	AA547959	Hs.115833	Hs.115833:ESTs	5.07
	403218				5.07
	411142	NM_014258	Hs.69009	NM_014258:Homo sapiens UDP-GlcNAc:beta-Ga	5.09
55	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.98
	433083	AL042769	Hs.191762	Hs.191762:hypothetical protein MGC20258	4.96
	431779	AW871178	Hs.268571	(locustink)NM_001645:Homo sapiens apolip	4.92
	421408	AJ688223	Hs.91095	NM_052816:Homo sapiens tripartite motif-	4.91
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.91
	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.90
60	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-proteoglycan	4.86
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25-dihydroxyvitami	4.83
	425983	AJ000228	Hs.165819	NM_031285:Homo sapiens mucin and cadheri	4.81
65	428289	M26301	Hs.2253	Hs.2253:complement component 2	4.79
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	4.78
	409689	AW530041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.77
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	423164	AK000232	Hs.124835	NM_019082:Homo sapiens hypothetical prot	4.72
70	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	4.72
	430680	AW138724	Hs.168974	Hs.168974:ESTs	4.69
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.69
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fl	4.67
	403221				4.65
75	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	4.65
	433437	U20536	Hs.3280	NM_001228:Homo sapiens caspase 6, apopto	4.64
	414062	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	4.64
	406673	M34998	Hs.198253	Hs.198253:major histocompatibility comp	4.64
	418203	X54942	Hs.53758	NM_001827:Homo sapiens CDC28 protein kin	4.60
80	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.60
	410639	BE268047	Hs.65234	(locustink)NM_017895:Homo sapiens DEAD/H	4.60
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, proper	4.59
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.57
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.56

5	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	4.54
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
10	408194	AA601038	Hs.181797	Hs.191797:ESTs	4.52
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
	420981	LA0904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
	432378	AM93046	Hs.146133	Hs.146133:ESTs	4.48
15	431958	XG3829	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
	415099	AI92170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
	422511	AL076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	435469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
20	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis	4.44
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.43
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.40
25	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MCC:23688	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
	439453	BE264874	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.35
30	408231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
	432575	AA553722	Hs.194346	Hs.194346:Spn-2 protein	4.33
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.33
	439983	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.32
35	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Dros	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
40	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.29
	422163	AF072208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	4.28
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inositol biphosph	4.27
45	414361	AA086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
	416827	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.22
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
50	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
	421606	BE302786	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.18
	408142	AL136877	Hs.50768	Hs.50768:SMC4 structural maintenance of	4.18
55	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding case	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncogene receptor inducing	4.17
	408113	TB2427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
	425743	BE396495	Hs.158428	NM_138781:Homo sapiens BCL2-associated X	4.15
	463751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.15
60	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.14
	403219				4.14
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
65	409956	AW103364	Hs.727	NM_002182:Homo sapiens inhibin, beta A (4.12
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.11
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.10
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.09
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
	425247	NM_006940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
75	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
	412812	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.04
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
80	462721	AJ269520	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
	459906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78998	NM_002592:Homo sapiens proliferating cel	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antigen	3.97
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
10	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
	431836	AF178532	Hs.271411	NM_136992:Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	227068	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
15	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to sknler	3.93
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	3.92
	456529	AW891966	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
20	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.90
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomulas	3.89
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	3.88
25	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AA85516	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
30	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	3.86
	434263	N34895	Hs.79187	Hs.79187:coxsaacke virus and adenovirus	3.85
	444700	NM_003845	Hs.11729	NM_003845:Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	3.84
	418526	BE015020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	3.84
	426898	AU076629	Hs.185950	NM_002011:Homo sapiens fibroblast growth	3.84
35	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.83
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
40	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	3.81
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030574:Homo sapiens solute	3.81
	407786	AA687638	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11982	NM_030766:Homo sapiens apoptosis regulat	3.79
45	414561	AID64813	Hs.195155	Hs.195155:solute carrier family 38, memb	3.79
	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens tranai	3.79
	400529				3.79
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
50	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
	429638	A1916682	Hs.211577	(locuslink)NM_004966:Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.77
	443639	BE289042	Hs.9881	Hs.9881:proteasome (prosome, macropain)	3.76
55	400290	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens tranai	3.76
	431350	A192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.75
	435099	AC004770	Hs.4766	NM_004411:Homo sapiens flap structure-sp	3.75
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	3.74
60	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.73
	420665	AW489240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
	444864	N26382	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.72
65	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	449437	AJ702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427480	Z95152	Hs.176695	NM_002754:Homo sapiens mitogen-activated	3.71
70	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
75	437016	AL076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.69
	430387	AW372804	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
80	413613	M96958	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
	426376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
	431890	X17033	Hs.271986	NM_002203:Homo sapiens Integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	418978	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acil	3.67

5	452679	Z42387	Hs.83683	(locuslink)NM_020182:Homo sapiens transmembrane protein 17 (TMEM17)	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	A1375726	Hs.227152	NM_016391:Homo sapiens hypothetical protein	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap)	3.66
	413095	AA494369	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.64
	404826				3.63
10	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	A1858183		BF755039:QV0-CT0563-181000-426-f07 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protein	3.61
15	439223	AW258299	Hs.250818	NM_025217:Homo sapiens UL16 binding protein	3.60
	408137	A1694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	A169355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449657	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
20	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcino	3.58
	424534	D87582	Hs.150275	Hs.150275:KIAA0241 protein	3.58
	428031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens displa	3.58
	417526	AA588906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N26522	Hs.8935	NM_014298:Homo sapiens quinoxaline phosph	3.57
25	424154	AF026004	Hs.141680	NM_004366:Homo sapiens chloride channel	3.57
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.56
	413880	A1660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.55
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.55
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.55
30	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.55
	420182	BE378432	Hs.95577	NM_062984:Homo sapiens cyclin-dependent	3.55
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413688	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.54
35	431542	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
	435777	AW419202	Hs.286192	NM_032182:Homo sapiens protein phosphata	3.54
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.53
	414812	X72755	Hs.77357	NM_002416:Homo sapiens monokine induced	3.53
40	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	3.53
	443180	R15875	Hs.258676	NM_012129:Homo sapiens claudin 12 (CLDN1	3.53
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
45	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.52
	412641	M16680	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.51
	409213	U61412	Hs.51133	NM_005875:Homo sapiens PTK6 protein tyro	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.51
	447200	BE543148	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ331373 fis	3.51
50	406683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	3.51
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	3.51
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisiae	3.51
	411678	A1907114	Hs.71465	NM_003128:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35876 fis	3.51
55	419693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion tra	3.51
	407971	A169117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-II	3.50
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antigen	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	438014	AF281134	Hs.283741	NM_020168:Homo sapiens exosome component	3.50
60	436278	BE398290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.50
	426788	AF082283	Hs.183516	NM_003921:Homo sapiens B-cell CLL/lympho	3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.49
65	417129	A1381800	Hs.300684	Hs.300684:calcitonin gene-related peptide	3.49
	409463	A458185	Hs.17286	NM_023930:Homo sapiens hypothetical prot	3.48
	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	438485	V57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.48
70	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.47
	446946	A1878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.47
	413980	A1904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	A1272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	438127	W94824	Hs.11585	NM_080748:Homo sapiens chromosome 20 ope	3.45
75	407770	AW807831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.45
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.98593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	AL048761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.44
80	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.43
	426459	AF151812	Hs.169992	NM_015986:Homo sapiens serologically def	3.43
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mal transforming	3.43
	428093	AW594508	Hs.104830	Hs.104830:ESTs	3.43

	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.43
	400750				3.42
5	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	3.41
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	3.40
	453957	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.40
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.39
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.39
	428206	AB020643	Hs.183008	Hs.183008:likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.39
	413179	N93692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.38
	440576	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.38
	400847				3.37
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	3.37
15	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	3.37
	432633	AI796390	Hs.210867	Hs.210867:ESTs	3.36
	429344	R94038	Hs.374664	NM_005638:Homo sapiens inhibin, beta C (3.36
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.36
	456950	AF111170	Hs.308165	Hs.308165:ESTs, Highly similar to unknow	3.35
20	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.35
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.35
	400448				3.35
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.35
25	430720	U85768	Hs.247836	NM_002991:Homo sapiens small inducible c	3.35
	418412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.35
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.34
30	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.34
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.34
	448093	AW977882	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.34
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.34
35	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.33
	435976	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.33
	418418	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.33
	433570	AI580563	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.33
40	441128	AA570255	Hs.348504	Hs.348504:hypothetical protein BC014072	3.33
	432320	AW411088	Hs.274351	NM_018032:Homo sapiens zinc finger, DHHC	3.33
	444019	BE173977	Hs.10088	NM_019082:Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens inter	3.32
	410219	T98228	Hs.171952	Hs.171952:occludin	3.32
45	410563	AA194852	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.32
	402829				3.32
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.32
	414188	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	3.32
	443425	AI058776	Hs.133397	Hs.133397:ESTs	3.32
50	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.31
	410288	AA316181	Hs.61835	NM_012449:Homo sapiens six transmembrane	3.30
	425169	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.30
	420614	AL110291	Hs.99364	Hs.99364:atthiolase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.30
	409402	AF208234	Hs.695	Hs.695:cystatin B (stafin B)	3.30
	421038	AL080182	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.29
	424408	AI754813	Hs.145428	Hs.145428:collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_002452:Homo sapiens nucleix (nucleoside	3.29
60	442621	BE391829	Hs.8752	Hs.8752:transmembrane protein 4	3.29
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422258	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.28
	408089	H58799	Hs.42644	Hs.42644:thioredoxin-like 2	3.28
65	432078	BE314877	Hs.24563	(locuslink)NM_022369:Homo sapiens hypothi	3.27
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.27
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.27
	414388	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.27
70	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, prota	3.26
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22959	3.26
	431183	NM_006855	Hs.250698	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.26
	457635	AV680378	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.26
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.25
75	417840	D30857	Hs.82353	NM_005404:Homo sapiens protein C recepto	3.25
	440088	NM_005402	Hs.6906	NM_005402:Homo sapiens v-rat simian leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.25
80	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.25
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.25
	447250	AU878909	Hs.17683	NM_002707:Homo sapiens protein phosphata	3.25
	452876	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.24
	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.24
	425811	AL039104	Hs.159557	NM_002268:Homo sapiens karyopherin alpha	3.24

5	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
	428858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
10	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE288621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-1	3.23
	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens nullid	3.23
	418881	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
15	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
	420186	NM_015926	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	AI272727	Hs.249163	NM_024308:Homo sapiens fatty acid hydrox	3.22
	448153	Y10805	Hs.20521	NM_001636:Homo sapiens HMT1 hnRNP methyl	3.22
	425274	BE281191	Hs.155462	Hs.155462:MCM5 minichromosome maintenanc	3.21
20	435472	AW972330	Hs.293022	NM_018843:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
25	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.20
	400263		Hs.75309	NM_001861:Homo sapiens eukaryotic transl	3.20
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	XS7522	Hs.352016	NM_008593:Homo sapiens transporter 1, AT	3.20
30	413431	AW248428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
	437379	AL358575	Hs.23785	Hs.23785:membrane metallo-endoropeptidase-	3.19
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfactant 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_005470:Homo sapiens tripep	3.19
35	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal gluta	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens Interleukin 2 rec	3.18
	428028	US2112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.18
	445580	AF167572	Hs.12912	NM_008109:Homo sapiens SKB1 homolog (S	3.18
	420531	AI852069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
40	417389	BE260964	Hs.82045	Hs.82045:mikdline (neurite growth-promoti	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	AI859380	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.18
	414883	AA269680	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.18
45	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.18
	447698	AI420166	Hs.326739	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
50	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.17
	425244	AK002127	Hs.155313	NM_022106:Homo sapiens death associated	3.16
	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
55	447151	AI022813	Hs.92679	(locuslink)NM_145754:Homo sapiens kines	3.15
	418862	BE550964	Hs.89389	NM_005176:Homo sapiens ATP synthase, H+	3.15
	410836	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
	435586	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
60	458778	AW451034	Hs.328525	NM_001689:Homo sapiens arylsulfatase D (3.14
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428371	AB012193	Hs.183874	NM_003699:Homo sapiens cullin 4A (CUL4A)	3.14
	450590	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXD d	3.14
	413900	AW409747	Hs.75612	NM_006818:Homo sapiens stress-induced-ph	3.13
65	406698	XQ3068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	447321	AW271217	Hs.261434	Hs.261434:Homo sapiens cDNA FLJ31373 fis	3.13
	426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
70	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	439778	AL109729	Hs.98364	Hs.98364:abhydrolase domain containing 1	3.12
	412328	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens etc family associ	3.12
75	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	AI879159	Hs.108219	NM_004528:Homo sapiens wingless-type MMT	3.11
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
80	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
	433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
	418641	BE243136	Hs.86947	NM_001108:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.108196	(locuslink)NM_016579:Homo sapiens BD6 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
	457670	AF119686	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

5	438407	AI457122	Hs.129673	Hs.129873:eukaryotic translation Initiat	3.10
	428293	BE250944	Hs.183556	Ha.183556:solute carrier family 1 (neur	3.10
	436823	AW749865	Hs.117077	Ha.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22265	Ha.22265:pyruvate dehydrogenase phosphat	3.10
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Ha.201076:ESTs	3.09
	427648	AI376722	Hs.180062	Ha.180062:proteasome (prosome, macropain	3.08
	404240				3.08
10	408989	AW361666	Hs.49500	Ha.49500:KIAA0746 protein	3.08
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
15	429671	BE379336	Hs.211594	Ha.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002998:Homo sapiens syndecan 4 (amph	3.07
	422811	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.07
	427647	W19744	Hs.180059	Ha.180059:Homo sapiens cDNA FLJ31360 fin	3.07
20	449644	AW900707	Hs.148324	Ha.148324:ESTs	3.07
	448719	AA033627	Hs.21858	Ha.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Ha.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	464128	AI031259	Hs.357900	Ha.357900:programmed cell death 2	3.07
25	424927	AW973666	Hs.153850	Ha.153850:hypothetical protein C321D2.4	3.07
	428144	BE269243	Hs.182625	Ha.182625:VAMP (vesicle-associated membr	3.07
	428440	BE382756	Hs.169902	NM_005516:Homo sapiens solute carrier fa	3.06
	428410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006596:Homo sapiens solute carrier fa	3.06
30	435750	AB029012	Hs.4990	Ha.4990:KIAA1089 protein	3.06
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.06
	421905	AI660247	Hs.32699	Ha.32699:Homo sapiens. Similar to RIKEN	3.06
	430642	AI557486	Hs.119122	Ha.119122:ribosomal protein L13a	3.06
	427288	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
35	412525	AA581439	Hs.152328	Ha.152328:ESTs	3.06
	422813	AV558571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.05
	441406	Z45957	Hs.7837	Ha.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Ha.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Ha.4984:KIAA0828 protein	3.05
40	432871	NM_016142	Hs.279517	Ha.279517:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z48223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	405353				3.05
45	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannosyl-P-dolicho	3.05
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-II	3.04
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	3.04
	439246	AM98072	Hs.351474	Ha.351474:Homo sapiens cDNA FLJ30092 fis	3.04
50	419493	AF001212	Hs.90744	Ha.90744:proteasome (prosome, macropain)	3.04
	427597	D15049	Hs.178770	NM_002842:Homo sapiens protein tyrosine	3.04
	430281	AI870842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.04
	452885	AI824046	Hs.119567	Ha.119567:ESTs, Weakly similar to ALU1_H	3.04
55	422164	NM_014312	Hs.112377	Ha.112377:cortical thymocyte receptor (X	3.04
	444301	AK000196	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepdlin antinuric	3.03
	417777	AI823763	Hs.7055	Ha.7055:Homo sapiens cDNA FLJ33420 fis	3.03
60	417144	AA382104	Hs.81337	Ha.81337:lectin, galactoside-binding, so	3.03
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	408430	R21945	Hs.346735	Ha.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
65	432268	BE311856	Hs.274230	Ha.274230:3'-phosphoadenosine 5'-phospho	3.03
	436930	AW843633	Hs.343261	Ha.343261:histocompatibility (minor) 13	3.02
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.02
	428788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related	3.02
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110906	Ha.110906:hypothetical protein BC004501	3.02
70	431236	AV656840	Hs.285115	NM_001560:Homo sapiens Interleukin 13 re	3.02
	414702	L22005	Hs.76832	NM_004359:Homo sapiens cell division cyc	3.02
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Ha.146381:RNA binding motif protein, X c	3.01
	442993	BE018882	Hs.166196	Ha.166196:ATPase, Class I, type 8B, memb	3.01
75	437712	X04588	Hs.85844	Ha.85844:neurotrophic tyrosine kinase, r	3.01
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.01
	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014611	Hs.70604	Ha.70604:ATPase, Class II, type 9A	3.00
80	447032	AI000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279829	(locuslink)NM_017610:Homo sapiens gp25L2	3.00
	448440	AA173467	Ha.62402	Ha.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1824	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Ha.90572:PTK7 protein tyrosine kinase 7	3.00
	417678	U90916	Hs.82845	Ha.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

5	431884	AAS21246	Hs.210792	Hs.210782:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
10	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, rbo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
	432996	AW295956	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
15	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	440913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
	414013	AA766505	Hs.47089	NM_024642:Homo sapiens hypothetical prot	2.98
20	462124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens nuclein 1, transmem	2.97
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437298	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
25	407736	N41744	Hs.349328	Hs.349328:Homo sapiens cDNA FLJ30877 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002256:Homo sapiens lamin	2.97
	430354	AA964810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
30	425221	AV849884	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33445	Hs.75799	Hs.75799:protease, serine, 8 (protease)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kines	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
35	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	429781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
40	445350	AF062112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
	429697	NM_003816	Hs.2442	Hs.2442:alpha disintegrin and metalloprotein	2.95
	421179	U72684	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
45	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
50	428583	NM_008412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.178703	NM_014788:Homo sapiens tripartite motif	2.94
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolchyl-diphosph	2.94
	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	2.94
	444824	AA843575	Hs.12068	NM_001671:Homo sapiens asialoglycoprotei	2.94
55	431829	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU078811	Hs.154672	Hs.154672:methylene tetrahydrofolate de	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA151527	Hs.69485	(locuslink)NM_024861:Homo sapiens hypoth	2.93
60	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.92
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
65	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
	451608	AA384525	Hs.26745	NM_016499:Homo sapiens H6PC244 (MGC:1337	2.92
	434608	AA805443	Hs.179809	NM_024831:Homo sapiens nuclear receptor	2.92
70	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	2.91
75	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PKA) a	2.91
	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
	408815	AW957974	Hs.25485	(locuslink)NM_024598:Homo sapiens hypoth	2.91
80	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonio	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	2.91
	422197	AW974265	Hs.111632	Hs.111632:Lim3 protein	2.90
	432710	AA809685	Hs.278572	NM_005898:Homo sapiens membrane componen	2.90
	405203			NM_005898:Homo sapiens membrane componen	2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.90
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90

	455967	L12535	Hs.75551	(locuslink)NM_012425: Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004: Homo sapiens farnes	2.90
	442739	NM_007274	Hs.8679	(locuslink)NM_007274: Homo sapiens cyto	2.90
5	456157	AW979153	Hs.336881	Hs.336881: ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274: Homo sapiens a disintegrin and	2.89
	430587	NM_003028	Hs.244542	Hs.244542: Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991: Homo sapiens ribosomal protein	2.89
10	438543	AA810141	Hs.192182	Hs.192182: ESTs	2.89
	426168	NM_001982	Hs.199067	NM_001982: Homo sapiens v-erb-b2 erythro	2.89
	441456	AJ271671	Hs.7854	NM_014437: Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339: Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797: Homo sapiens proteasome (proso	2.89
	409591	AA532963	Hs.9100	Hs.9100: hypothetical gene supported by A	2.89
15	418062	AW630656	Hs.83383	NM_006406: Homo sapiens peroxiredoxin 4 (2.89
	436540	BE397032	Hs.14468	NM_020230: Homo sapiens pater pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122: hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887: v-yes-1 Yamaguchi sarcoma viral	2.89
	421684	BE291591	Hs.106768	NM_018120: Homo sapiens hypothetical prot	2.88
20	429404	NM_005738	Hs.10706	NM_005738: Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346: Homo sapiens opifol	2.88
	413822	R08950	Hs.272044	Hs.272044: ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967: ESTs, Weakly similar to extensin	2.88
	409132	AJ224538	Hs.50732	NM_005399: Homo sapiens protein kinase, A	2.88
25	440490	AW513684	Hs.7218	Hs.7218: acetyl-Coenzyme A synthetase 2 (2.87
	431498	AK001777	Hs.258551	NM_012100: Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344: Homo sapiens hypothetical prot	2.87
	448689	BE382657	Hs.21486	Hs.21486: signal transducer and activator	2.87
	451711	AK000461	Hs.26890	NM_017829: Homo sapiens cat eye syndrome	2.87
30	442643	U82758	Hs.374973	(locuslink)NM_004697: Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228: Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419: zinc finger protein	2.87
	443329	BE282943	Hs.9234	NM_032635: Homo sapiens seven transmembra	2.87
	416448	L13210	Hs.79339	NM_005567: Homo sapiens lectin, galactosyl	2.87
35	453145	R63438	Hs.183464	Hs.183464: Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R28944	Hs.180777	Hs.180777: Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D80001	Hs.152629	Hs.152629: KIAA0179 protein	2.86
	426125	X87241	Hs.168994	Hs.168994: FAT tumor suppressor homolog 1	2.86
40	450273	AW296464	Hs.24743	Hs.24743: hypothetical protein FLJ20171	2.86
	407082	Z47056			2.86
	450038	AA005159	Hs.188489	Hs.188489: ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391: Homo sapiens hypothetical prot	2.85
	417831	H16423	Hs.82686	Hs.82686: CD47 antigen (Rb-related antigen	2.85
45	417824	AA084788	Hs.82646	NM_006145: Homo sapiens DnaJ (Hsp40) homo	2.85
	426989	A1815206	Hs.100293	Hs.100293: O-linked N-acetylglucosamine (2.85
	434916	AF161383	Hs.284207	Hs.284207: hypothetical protein BC003515	2.85
	412664	AA421404	Hs.346868	NM_006824: Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locuslink)NM_002642: Homo sapiens phosph	2.85
50	408504	AA304961	Hs.698	Hs.698: peptidylprolyl isomerase B (cyclo	2.84
	439920	H05430	Hs.288433	NM_016522: Homo sapiens neurotrophin (HNT)	2.84
	418462	BE001596	Hs.85266	Hs.85266: Integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879: Homo sapiens etoposide-induced	2.84
	406710	A1708347	Hs.184014	Hs.184014: ribosomal protein L31	2.84
	433435	BE645277	Hs.340959	NM_005726: Homo sapiens Tc translation ef	2.84
55	415402	AA164687	Hs.177576	Hs.177576: mannosyl (alpha-1,3)-glycopro	2.84
	448730	A9092983	Hs.21894	Hs.21894: KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locuslink)NM_014366: Homo sapiens putail	2.84
	449090	AK001735	Hs.22983	NM_020121: Homo sapiens UDP-glucose coram	2.84
60	439737	A1751438	Hs.41271	Hs.41271: Homo sapiens mRNA full length i	2.84
	403912				2.84
	423225	AA852804	Hs.125358	NM_006288: Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059: KIAA0982 protein	2.84
	429211	AF052683	Hs.198249	NM_005268: Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24758	Hs.24758: Homo sapiens cDNA FLJ32068 fis	2.84
	418127	BE243982	Hs.83532	(locuslink)NM_002388: Homo sapiens membra	2.83
	448499	A1823875		R45782: Ha616-f Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.20001	NM_001061: Homo sapiens thromboxane A syn	2.83
	422129	AU076835	Hs.1478	NM_000185: Homo sapiens serine (or cyste)	2.83
70	437651	BE560672	Hs.13543	(locuslink)NM_145214: Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059: Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882: Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000859: Homo sapiens 3-hydroxy-3-methyl	2.83
	423323	A1851628	Hs.127007	NM_003740: Homo sapiens potassium channel	2.83
75	439720	A1935202	Hs.31181	Hs.31181: Homo sapiens cDNA: FLJ23230 fis	2.83
	435550	AJ224456	Hs.324507	Hs.324507: hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155865	Hs.155865: ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159: bifunctional apoptosis regulat	2.82
	427640	AF068293	Hs.180015	NM_001355: Homo sapiens D-dopachrome taut	2.82
80	433233	AB040927	Hs.301804	Hs.301804: KIAA1494 protein	2.82
	415997	A1365603	Hs.279698	Hs.279698: DKFZP6661024 protein	2.82
	441321	H17182	Hs.77771	NM_007273: Homo sapiens repressor of asir	2.82
	430040	AW503115	Hs.227823	NM_014287: Homo sapiens pM5 protein (PM5)	2.82
	449854	AA641636	Hs.37477	Hs.37477: ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004696:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
5	418501	AW843822	Hs.169961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
	418140	BE613536	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_018310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201831	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_008280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin 1 (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
	410240	AL157424	Hs.61289	Hs.61289:synaptobrevin 2	2.80
	423680	BE278111	Hs.134200	Hs.134200:DKFZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001825:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456902	AA411607	Hs.118964	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076637	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	2.79
	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021897:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419848	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
30	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Nt56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001882:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
35	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1808 protein	2.79
	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrophin (HNT)	2.78
	407754	AA527348	Hs.288957	Hs.288957:Homo sapiens, similar to RIKEN	2.78
	422282	AF018225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AI000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418869	AW516565		AA229762:nc49701.r1 NCL CGAP_Py3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430260	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
45	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
50	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
	409932	AI376760	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206939	Hs.42287	NM_001852:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	446960	AA305800	Hs.6672	(locuslink)NM_030799:Homo sapiens golgi	2.77
	444207	AI660004	Hs.374416	Hs.374416:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24963	Hs.24963:hypothetical protein from EUROI	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412990	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAS20, member RAS	2.76
	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419584	AA013051	Hs.91417	(locuslink)NM_007027:Homo sapiens topoi	2.76
	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acyl-coA:acyl hydro	2.76
70	439888	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
	426520	BE545584	Hs.343566	Hs.343566:KIAA0251 protein	2.76
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV852402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
	428157	AI738719	Hs.198427	NM_000185:Homo sapiens hexokinase 2 (HK2	2.75
75	416178	AI808527	Hs.192822	NM_030948:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAAP1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57803	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
80	408196	AL034548	Hs.43827	NM_008943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.74

	423627	AI206965	Hs.105861	(locuslink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	2.74
5	450247	AF123303	Hs.24713	NM_013388:Homo sapiens hypothetical prot	2.74
	422891	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	2.74
	440457	BE387593	Hs.21321	(locuslink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
10	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183563	NM_030666:Homo sapiens serine (or cyste)	2.73
	421921	H83353	Hs.355993	NM_012455:Homo sapiens translocase of in	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to chol	2.73
15	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400276		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synth	2.73
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
20	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
	436895	AI180015	Hs.125489	Hs.125489:KIAA1981 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
25	445899	AI263736	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
	453557	AA622464	Hs.285995	NM_024956:Homo sapiens hypothetical prot	2.72
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA570635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
30	428466	AF151083	Hs.184456	NM_018486:Homo sapiens hypothetical prot	2.71
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	2.71
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	2.71
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
35	415169	WA2913	Hs.78069	NM_004231:Homo sapiens ATPase, H+ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
	428263	AI908774	Hs.259785	Hs.259785:camitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
40	441238	AI372655	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
	424955	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412873	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
45	410113	AW996564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.70
	447098	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	2.70
	450493	M83718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endo	2.70
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
50	436042	AF284422	Hs.118178	(locuslink)NM_020246:Homo sapiens cation	2.70
	432981	NM_002733	Hs.3135	Hs.3135:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43686	NM_007079:Homo sapiens protein tyrosine	2.70
55	416770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H58688	Hs.18747	NM_006837:Homo sapiens POP7 (processing	2.70
	424500	AF040704	Hs.149443	(locuslink)NM_007022:Homo sapiens putab	2.69
	414237	BE536554	Hs.278270	Hs.278270:inactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
60	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCL CGAP_Pr2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
65	448957	D31365	Hs.24220	(locuslink)NM_016479:Homo sapiens scotin	2.69
	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domain	2.69
	429544	BE299343	Hs.2430	NM_005897:Homo sapiens transcription fac	2.68
	428582	BE336689	Hs.185055	Hs.185055:BENE protein	2.68
70	445139	AB037848	Hs.12366	Hs.12366:cytoskeleton XIII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
	416883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD/H (Asp-Glu-Ala-Asp)-f	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntaxin 4A (plac	2.68
75	409533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of ou	2.68
	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
80	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paroxonase 2 (PO	2.67
	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450628	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 proteas	2.67
	433339	AF019226	Hs.8036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
	427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
5	415116	AA160363	Hs.269956	Hs.269956:ESTs	2.67
	425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
	418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
	410165	BE580228	Hs.71889	NM_013258:Homo sapiens apoptosis-associ	2.66
	410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
10	430066	AJ929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
	429910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
	427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxin 1 (MTX1),	2.66
	439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
	438449	AK001333	Hs.8216	Hs.8216:DnaJ (Hsp40) homolog, subfamily	2.66
15	435906	AJ683379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
	433387	L76528	Hs.3250	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
	447191	NM_014521	Hs.17567	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
	444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
20	418529	AW005895	Hs.250897	Hs.250897:TRK-fused gene	2.65
	426026	AW136330	Hs.17658	Hs.17658:Homo sapiens, clone IMAGE:40704	2.65
	420187	AK001714	Hs.95744	NM_018028:Homo sapiens hypothetical prot	2.65
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
	444395	N86148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida g	2.65
	406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
	440708	AF088962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65
	418526	H61082	Hs.14743	Hs.14743:ESTs	2.65
	413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (brai	2.65
30	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
	452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transport	2.65
	406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31253	2.64
	451295	AJ557212	Hs.17132	Hs.17132:ESTs	2.64
35	448428	AF282874	Hs.21201	NM_015480:Homo sapiens necln 3 (DKFZP56	2.64
	426611	BE178050	Hs.171271	NM_001904:Homo sapiens cadherin (cadherin	2.64
	426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
	407223	H96850		H96850:yu03b12.s1 Soares melanocyte 2Nbh	2.64
	427725	U66839	Hs.180533	NM_002758:Homo sapiens mitogen-activated	2.64
40	420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
	428471	X67348	Hs.184510	Hs.184510:estradiol	2.64
	451644	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
	413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64
	415020	BE243915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
45	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
	418684	U82587	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
	410668	BE379794	Hs.159851	NM_014452:Homo sapiens tumor necrosis fa	2.64
	438183	AJ146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
	412228	BE563042	Hs.118820	Hs.118820:hypothetical protein BC007882	2.64
50	432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
	432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64
	450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
	434633	AJ189587	Hs.120915	Hs.120915:ESTs	2.64
	424707	BE051914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
55	427600	AW630918	Hs.178774	Hs.178774:proteasome (prosome, macropain	2.63
	446522	NM_003876	Hs.15198	NM_003876:Homo sapiens putative receptor	2.63
	436906	H95890	Hs.181244	Hs.181244:major histocompatibility compl	2.63
	410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
	410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
60	408716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
	430308	BE540865	Hs.238990	NM_004084:Homo sapiens cyclin-dependent	2.63
	431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
	412867	AJ076861	Hs.74637	Hs.74637:leafe enhanced gene transcript	2.63
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
65	435968	AW181481	Hs.111577	(locuslink)NM_030526:Homo sapiens Integr	2.63
	422672	X12784	Hs.118129	NM_001845:Homo sapiens collagen, type IV	2.63
	447528	AJ612027	Hs.75277	NM_138393:Homo sapiens hypothetical prot	2.63
	406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
	439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
70	435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
	428689	AW578252	Hs.190181	Hs.190181:LR8 protein	2.62
	410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
	414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
	443217	NM_001545	Hs.9078	Hs.9078:Immature colon carcinoma transcr	2.62
75	448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
	450009	AJ399947	Hs.168486	Hs.168486:Homo sapiens cDNA FLJ11432 fis	2.62
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
	442232	AJ357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
80	416114	AJ695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
	439437	AJ207788	Hs.343628	Hs.343628:glucuronidase 4B (beta-gal	2.61
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
	443142	AJ696513	Hs.108705	Hs.108705:protein phosphatase 2 (formerl	2.61
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419667	AL077005	Hs.92208	NM_003815: Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876: hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301: hypothetical protein MGC13170	2.61
	403399				2.61
5	419679	W49529	Hs.296200	NM_023948: Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481: ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984: Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180: DC2 protein	2.61
	446488	AB037782	Hs.15119	Hs.15119: KIAA1361 protein	2.61
10	442504	BE503373	Hs.334335	NM_022484: Homo sapiens hypothetical prot	2.60
	448204	AJ475124	Hs.170561	Hs.170561: ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280: Homo sapiens FtsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509: ESTs, Weakly similar to C3HU com	2.60
	424805	AF230904	Hs.153260	NM_031892: Homo sapiens SH3-domain kinase	2.60
15	425421	L11669	Hs.157145	Hs.157145: tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069: Homo sapiens adapto	2.60
	460858	C18458	Hs.25597	Hs.25597: elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063: Homo sapiens cDNA FLJ14201 fis	2.59
	430604	H52761	Hs.44095	Hs.44095: cyclin M3	2.59
20	439678	AW283124	Hs.350547	NM_024665: Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647: Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239: zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521: Homo sapiens general transcrip	2.59
	422140	BE295918	Hs.112193	(locuslink)NM_025259: Homo sapiens chromo	2.59
25	452817	AA322859	Hs.284275	Hs.284275: p21 (CDKN1A)-activated kinase	2.59
	413953	AW293542	Hs.75309	Hs.75309: eukaryotic translation elongati	2.59
	421700	BE515018	Hs.107014	NM_016641: Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66483	NM_016430: Homo sapiens Down syndrome cri	2.59
30	440511	AF132859	Hs.7236	NM_015953: Homo sapiens eNOS interacting	2.59
	407887	AA579668	Hs.41072	(locuslink)NM_004568: Homo sapiens serine	2.59
	425356	BE244879	Hs.165939	NM_005541: Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.821	Hs.821: lectin, galactoside-binding, solu	2.59
	417952	AI92838	Hs.173135	Hs.173135: dual-specificity tyrosine-(Y)-	2.59
35	433053	BE301909	Hs.279952	NM_015917: Homo sapiens glutathione S-tra	2.59
	450935	BE514743	Hs.379039	NM_005851: Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959: Homo sapiens protel	2.59
	438364	AK000860	Hs.6191	NM_020441: Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550: Homo sapiens chromosome 20 ope	2.58
40	444838	AV651680	Hs.208558	Hs.208558: ESTs	2.58
	416435	AA31301	Hs.374897	Hs.374897: Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452: solute carrier family 20 (phosp	2.58
	452222	AW808287	Hs.21432	Hs.21432: EX gene	2.58
	400541				2.58
45	444309	U83236	Hs.10803	Hs.10803: calcium and Integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858: ribosomal protein L7a	2.58
	418629	BE247560	Hs.86859	(locuslink)NM_005310: Homo sapiens growth	2.58
	432995	AF105025	Hs.279801	Hs.279801: PTD009 protein	2.57
	428781	AL048967	Hs.172207	(locuslink)NM_007363: Homo sapiens non-PO	2.57
50	452636	BE615074	Hs.145279	Hs.145279: SET translocation (myeloid leu	2.57
	406851	AA609784	Hs.362392	Hs.362392: major histocompatibility comp	2.57
	447874	BE270640	Hs.19192	NM_001798: Homo sapiens cyclin-dependent	2.57
	445847	AV654627	Hs.271808	Hs.271808: Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824: Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI688139	Hs.202093	Hs.202093: ESTs	2.57
	414029	BE297731	Hs.76709	NM_002355: Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946: Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100: ESTs	2.56
60	449378	AW664026	Hs.59892	Hs.59892: ESTs, Weakly similar to alpha 5	2.56
	442599	AF076037	Hs.324051	(locuslink)NM_006663: Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21636	NM_001070: Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844: Homo sapiens protein tyrosine	2.56
	426044	AA083322	Hs.301404	NM_006743: Homo sapiens RNA binding motif	2.56
65	451664	AL076698	Hs.132760	(locuslink)NM_001467: Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	(locuslink)NM_145169: Homo sapiens simila	2.56
	439830	AA313607	Hs.58633	Hs.58633: Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.81343	NM_000807: Homo sapiens gamma-aminobutyl	2.55
	448279	BE250564	Hs.283655	Hs.283655: lysophospholipase II	2.55
70	453360	AI917771	Hs.61790	(locuslink)NM_024658: Homo sapiens import	2.55
	423720	AL044191	Hs.23388	NM_030817: Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087: Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205736	Hs.205736: KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584: ribosomal protein S6 kinase, 9	2.55
75	434848	BE256304	Hs.32148	NM_018445: Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	(locuslink)NM_017806: Homo sapiens hypoth	2.55
	449089	D78850	Hs.250465	Hs.250465: Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673: Homo sapiens SEC13-like 1 (S	2.55
	437469	AW753112	Hs.15514	Hs.15514: hypothetical protein MGC3260	2.55
80	407755	AI151353	Hs.29742	Hs.29742: Homo sapiens cDNA FLJ32147 fis	2.55
	446673	NM_016361	Hs.15871	NM_016361: Homo sapiens LPAP for lysophos	2.55
	411766	AA399871	Hs.71989	Hs.71989: Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943: natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874: Homo sapiens, clone MGC:31984	2.55

5	417785	X59812	Hs.82568	NM_000784: Homo sapiens cytochrome P450,	2.55
	443358	H65417	Hs.17757	(locuslink)NM_021622: Homo sapiens plectra	2.55
	452349	AB028944	Hs.29189	Hs.29189: ATPase, Class VI, type 11A	2.55
	427721	AI582843	Hs.180455	NM_005053: Homo sapiens RAD23 homolog A (2.54
	407559	AA313352	Hs.280858	Hs.280858: Homo sapiens cDNA FLJ32370 fis	2.54
10	413426	U88837	Hs.75354	Hs.75354: GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904: protein kinase C, tota	2.54
	444152	AI125694	Hs.149305	Hs.149305: hypothetical protein MGC2603	2.54
	451820	AW058357	Hs.199248	NM_000958: Homo sapiens prostaglandin E r	2.54
	441356	BE384361	Hs.182885	(locuslink)NM_004556: Homo sapiens nuclea	2.54
15	444410	BE387350	Hs.33719	Hs.33719: Homo sapiens, similar to data s	2.54
	415200	AL040828	Hs.78202	NM_003072: Homo sapiens SWI/SNF related,	2.54
	403955				2.54
	430361	AI033955	Hs.239926	Hs.239926: sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	Hs.274479	NM_013330: Homo sapiens NME7 (NME7), mRNA	2.54
20	445719	W39500	Hs.301872	Hs.301872: hypothetical protein MGC4840	2.54
	439841	AI392840	Hs.18272	NM_030574: Homo sapiens solute carrier fa	2.54
	436685	W28661	Hs.5288	Hs.5288: Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AL134847	Hs.149957	Hs.149957: ribosomal protein S6 kinase, 9	2.54
	442904	AW575008	Hs.11355	Hs.11355: thymopolein	2.54
25	422605	H16646	Hs.118666	Hs.118666: hypothetical protein PP591	2.54
	442069	AW654144	Hs.297007	Hs.297007: Homo sapiens cDNA FLJ32174 fis	2.54
	447382	AW176120	Hs.9061	NM_024099: Homo sapiens hypothetical prot	2.53
	416305	AJ076628	Hs.79187	NM_001338: Homo sapiens coxsackie virus a	2.53
	422624	BE618678	Hs.76152	NM_006854: Homo sapiens KDEL (Lys-Asp-Glu	2.53
30	447298	BE617527	Hs.239818	NM_006219: Homo sapiens phosphoinositide-	2.53
	412833	AW860547	Hs.298262	Hs.298262: ribosomal protein S19	2.53
	404854				2.53
	415761	AA132666	Hs.78802	(locuslink)NM_002093: Homo sapiens glyco	2.53
	431104	AW970859	Hs.313503	Hs.313503: ESTs	2.53
35	439180	AI393742	Hs.199067	Hs.199067: v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	Hs.143648	NM_003749: Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374: Homo sapiens cDNA FLJ31250 fis	2.53
	415742	BE410243	Hs.78769	NM_003249: Homo sapiens thimet oligopepti	2.53
	404140				2.53
40	407255	AA012992	Hs.256301	Hs.256301: hypothetical protein MGC13170	2.53
	422609	AA258513	Hs.117865	Hs.117865: solute carrier family 17 (anio	2.53
	434866	AW002565	Hs.355460	Hs.355460: Homo sapiens cDNA: FLJ121763 fi	2.53
	429743	AA804393	Hs.286985	(locuslink)NM_017961: Homo sapiens hypoth	2.53
	433047	M86135	Hs.279946	NM_004990: Homo sapiens methionine-tRNA s	2.53
45	418945	BE246762	Hs.89499	Hs.89499: arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433: Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784: prolactin regulatory element b	2.52
	448252	BE622791	Hs.12199	NM_030577: Homo sapiens hypothetical prot	2.52
	447365	BE383678	Hs.334	(locuslink)NM_005435: Homo sapiens Rho gu	2.52
50	414844	AA295874	Hs.77484	NM_080816: Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945: Homo sapiens ovarian cancer ov	2.52
	418149	AA311965	Hs.79058	NM_003168: Homo sapiens suppressor of Ty	2.52
	418741	H83265	Hs.8881	Hs.8881: Homo sapiens cDNA FLJ32153 fis,	2.52
	437952	D63209	Hs.5944	NM_014585: Homo sapiens solute carrier fa	2.52
55	445825	BE246743	Hs.353181	(locuslink)NM_025092: Homo sapiens hypoth	2.52
	431666	AF161470	Hs.280622	Hs.280622: butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718: Homo sapiens cell d	2.52
	431476	BE612705	Hs.256697	(locuslink)NM_006340: Homo sapiens histid	2.52
	406672	M26041	Hs.198253	(locuslink)NM_002122: Homo sapiens major	2.52
60	418180	BE618087	Hs.83724	Hs.83724: hypothetical protein MGC5488	2.52
	428248	AI126772	Hs.40479	Hs.40479: Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	AB020980	Hs.93632	Hs.93632: putative membrane protein	2.52
	446143	BE245342	Hs.308079	NM_013336: Homo sapiens protein transport	2.52
	426691	NM_008201	Hs.171834	(locuslink)NM_006201: Homo sapiens PCTAIR	2.51
65	408124	U89337	Hs.42853	NM_004381: Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651: Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638: polymerase (RNA) II (DNA direc	2.51
	414721	X90392	Hs.77091	NM_006730: Homo sapiens deoxyribonuclease	2.51
	422607	Z45471	Hs.118684	NM_005923: Homo sapiens stromal cell-deri	2.51
70	421846	AA017707	Hs.1432	NM_002743: Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224: Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959: Homo sapiens CGI-31 protein (L	2.51
	438393	AA351815	Hs.50740	Hs.50740: Homo sapiens mRNA; cDNA DKFZp76	2.51
	418360	AW296974	Hs.84264	NM_006401: Homo sapiens acidic (leucine-r	2.50
75	401061				2.50
	428559	AB001914	Hs.170414	Hs.170414: paired basic amino acid cleavi	2.50
	412204	AF125507	Hs.24937	Hs.24937: transformer-2 alpha (tra-2 alp	2.50
	448960	AF288687	Hs.9275	NM_020410: Homo sapiens CGI-152 protein (2.50
	408936	AK001681	Hs.57655	(locuslink)NM_018234: Homo sapiens dudul	2.50
80	414675	R79015	Hs.288968	Hs.288968: RAB22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012293: Homo sapiens Kelch-	2.50
	450914	AT743761	Hs.142528	Hs.142528: ESTs	2.50
	444630	AT753230	Hs.323562	(locuslink)NM_032121: Homo sapiens hypoth	2.50
	401353				2.50
	441680	AW444598	Hs.7940	(locuslink)NM_021158: Homo sapiens RAP1,	2.50
	406880	AA876469		AA876469: cce46b04.s1 NCI_CGAP_Pr25 Homo s	2.50
	448163	AW161356	Hs.23119	NM_003492: Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimerin (chimaerin) 2	2.50
430800	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	2.50

5 TABLE 9B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

10 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
452098	181393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 A056183
451129	1495511_1	BE072881 A1762181 BE072946
15 459305	223120_4	AW578452
448489	2189115_1	R45782 R45781
418869	12789_14	AA229762 AA230035
418546	242836_1	T69708 AA224827 T58843 BE166903
20 455303	1152492_1	BE068891 BE066895 AW892049 BE066897 BE903684
406860	0_0	AA876469

TABLE 9C

25 Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
406399	9256288	Minus	63448-63554
403220	7630969	Plus	84398-64517
403216	7630969	Plus	58039-58149
35 403221	7630969	Plus	66294-66438,66938-67124
403219	7630969	Plus	61858-61995
403739	7630862	Plus	44563-44766,46209-48483,52255-52495
405484	6922025	Plus	199214-199579,199672-199920,200262-20049
405556	1552511	Plus	163497-163823,164715-164958,165369-16550
40 406529	9796988	Plus	138232-138423
404826	6572184	Plus	47726-48046
400750	8119067	Plus	198891-199168,199316-199548
400847	9188605	Plus	44643-44835
400448	9887687	Minus	177372-177674
45 402829	8918414	Plus	101532-101852,102008-102263
400846	9188605	Plus	39310-39474
401170	9438647	Plus	113477-113883
404240	5002624	Minus	116132-116407,116853-116922
50 402260	3399865	Minus	113765-113910,115853-115765,116808-11694
406363	9256114	Plus	14403-14602,17000-17147,17241-17368
405203	7230116	Plus	125295-125463
402104	8119072	Plus	122409-122600
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
55 400845	9188605	Plus	34428-34612
403217	7630969	Plus	64089-64183,65427-55623
403483	9956168	Minus	144546-144854
400509	9796539	Minus	157909-168430
403399	6684178	Plus	61841-62145,62367-62756
60 400541	7674902	Plus	126235-126380,126478-126597
402861	2814308	Minus	14933-16231,15387-15627
403955	7770475	Minus	54527-54740
404854	7143420	Plus	14260-14537
404140	9843620	Plus	37761-38147
65 401081	3242744	Minus	99468-99549,100707-100848,100918-101107,
401353	9931295	Minus	50831-51352

70 Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymatrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 50th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75 TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

80 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
Rt: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	436749	AA584890	Hs.5302	NM_008149:Homo sapiens lectin, galactosi	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intesti	14.04
	431912	AI680552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	14.02
	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	13.72
10	408690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carc	13.44
	418406	X73501	Hs.84905	Hs.84905:cyclokeratin 20	12.70
	406657	M12623			12.42
	416768	AA363733	Hs.1032	NM_008507:Homo sapiens regenerating isle	11.98
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
15	422578	AF239566	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
20	441031	AI110884	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
	424212	NM_006814	Hs.143131	NM_006814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.572	Hs.572:corosomucoid 1	9.20
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carc	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
	430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
	409863	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small i	8.08
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.05
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (7.95
	436524	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
	410407	X88639	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.46
35	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
	412374	X01386	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
40	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carc	7.26
	414386	X00442	Hs.75980	NM_005143:Homo sapiens haptoglobin (HP),	7.21
	404519				7.18
	413585	AI133462	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
	430828	AI783257	Hs.86327	Hs.86327:homeo box B9	6.83
	433927	AI557019	Hs.116487	NM_032391:Homo sapiens small nuclear pro	6.81
	406587	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
	423538	AW803823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.63
50	434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
	409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
55	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
	420823	AF097021	Hs.273321	NM_005418:Homo sapiens differentially ex	5.94
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	5.90
60	420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to 610590	5.89
	431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
	432023	AW273128	Hs.300268	Hs.300268:EST	5.75
65	447033	AI357412	Hs.157601	Hs.157601:ESTs	5.69
	411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
	408885	M18728		(locuslink)NM_002483:Homo sapiens carc	5.55
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
	443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
70	408153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	5.44
	449368	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW012795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fis	5.38
	433013	AI897890	Hs.127337	(locuslink)NM_004855:Homo sapiens xln 2	5.38
	419079	AW014838	Hs.18844	Hs.18844:ESTs	5.37
75	428365	BE265452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	5.35
	422966	BE545072	Hs.122579	(locuslink)NM_018098:Homo sapiens epithe	5.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	5.30
	450543	AI394037	Hs.170295	Hs.170298:Homo sapiens cDNA: FLJ22090 fi	5.30
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 40	5.30
80	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
	411825	AK000394	Hs.352415	NM_017767:Homo sapiens solute carrier fa	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	5.21
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16

5	447208	BE315291	Hs.237971	NM_024096: Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004963: Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409: Homo sapiens small inducible c	5.07
	447342	A1199268	Hs.19322	Hs.19322: Homo sapiens, Similar to RIKEN	5.06
	452194	A1694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
	403220				4.94
10	408380	AF123050	Hs.44532	NM_006398: Homo sapiens ubiquitin D (UBD)	4.92
	415214	AM445236	Hs.125124	NM_004442: Homo sapiens EphB2 (EPHB2), tr	4.92
	431330	X68532	Hs.2777	NM_002215: Homo sapiens inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373: Homo sapiens putative G protei	4.84
15	452594	AL076405	Hs.29981	Hs.29981: scute carrier family 26 (scut)	4.81
	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
	444666	BE293347	Hs.11638	(locuslink)NM_016234: Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878: Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000442: Homo sapiens apolipoprotein H	4.80
20	455830	AV656701	Hs.76183	NM_000773: Homo sapiens cytochrome P450,	4.78
	422310	AA316622	Hs.98370	(locuslink)NM_030622: Homo sapiens cytoch	4.78
	423337	NM_004655	Hs.127337	NM_004655: Homo sapiens axin 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432: Homo sapiens epi-regulin (EREG)	4.73
	408908	BE256227	Hs.250822	(locuslink)NM_003158: Homo sapiens serine	4.70
25	423936	U77629	Hs.135639	NM_005170: Homo sapiens achaete-scute com	4.70
	404661				4.68
	408704	AA056635	Hs.5366	NM_139053: Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
30	451035	AL076785	Hs.430	NM_002670: Homo sapiens plastin 1 (l iso)	4.61
	427506	AK000134	Hs.179100	NM_017678: Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324: Homo sapiens alpha-methylacyl-	4.59
	453884	AA355925	Hs.36232	NM_021067: Homo sapiens KIAA0186 gene pro	4.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.64
	408983	NM_000492	Hs.663	NM_000492: Homo sapiens cystic fibrosis t	4.54
35	449032	AA045573	Hs.22900	NM_004289: Homo sapiens nuclear factor (a	4.54
	434540	NM_016045	Hs.3945	NM_016045: Homo sapiens chromosome 20 ope	4.54
	407242	M18728		(locuslink)NM_002483: Homo sapiens carcin	4.53
	453746	AI381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923: Homo sapiens cDNA: FLJ22785 f	4.51
40	424273	W04060	Hs.144442	NM_003581: Homo sapiens phospholipase A2,	4.50
	411975	AI916058	Hs.144583	Hs.144583: Homo sapiens, clone IMAGE:3462	4.49
	425371	D49441	Hs.155981	NM_005823: Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820: hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
45	419559	Y07828	Hs.91086	NM_007028: Homo sapiens tripartite motif-	4.44
	430294	AI538228	Hs.32976	(locuslink)NM_004485: Homo sapiens guanin	4.42
	411248	AA551538	Hs.69321	Hs.69321: KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083: Homo sapiens glutathione perox	4.37
50	434414	AI798376		AF134163: Homo sapiens Human endogenous r	4.36
	443426	AF088158	Hs.9329	(locuslink)NM_012112: Homo sapiens chromo	4.35
	422539	AJ009938	Hs.118138	NM_033013: Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640: occludin 3	4.33
	450631	AW301032	Hs.203800	Hs.203800:ESTs	4.33
55	403055				4.31
	414809	AI434689	Hs.77356	Hs.77356: transferrin receptor (p90, CD71	4.31
	400955				4.30
	430204	AA618335	Hs.356664	Hs.356664: hypothetical protein FLJ32334	4.29
60	432978	AF126743	Hs.279884	NM_013238: Homo sapiens DNAJ domain-conta	4.29
	417931	W95842	Hs.82951	Hs.82951: Homo sapiens, clone MGC:225881	4.28
	430832	AI073913	Hs.100586	Hs.100586: anterior gradient protein 3	4.28
	409482	NM_000676	Hs.45743	NM_000676: Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406: Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(locuslink)NM_025130: Homo sapiens hypoth	4.27
65	452940	AA029722	Hs.2173	NM_002033: Homo sapiens fucosyltransferas	4.27
	439211	AI890347	Hs.271923	Hs.271923: Homo sapiens cDNA: FLJ22785 f	4.27
	459299	BE094281	Hs.155551	NM_021784: Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113: Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.89009	NM_014256: Homo sapiens UDP-GlcNAc:beta-Ga	4.24
70	421777	BE582088	Hs.108196	NM_016095: Homo sapiens HSPC037 protein (4.21
	419396	BE258326	Hs.90280	Hs.90280: 5-aminoimidazole-4-carboxamide	4.20
	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280: chromosome 20 open reading fra	4.19
75	409757	NM_001898	Hs.123114	NM_001898: Homo sapiens cystatin SN (CST1	4.19
	426227	U67058	Hs.154299	(locuslink)NM_005242: Homo sapiens coagul	4.19
	421408	AM688223	Hs.91096	NM_052816: Homo sapiens bipartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297: Homo sapiens protein expressed	4.17
80	414075	U11862	Hs.75741	NM_001091: Homo sapiens amiloride binding	4.17
	444151	AW972917	Hs.128749	(locuslink)NM_014324: Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125808	Hs.125808:ESTs	4.16
	445654	AB028957	Hs.12896	Hs.12896: KIAA1034 protein	4.16
	424657	J05070	Hs.151738	NM_004994: Homo sapiens matrix metallopro	4.12

	401866				4.11
	431811	U58766	Hs.264428	Hs.264428:tissue specific transplantaio	4.10
	430187	AF199909	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37836 fis	4.10
5	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	4.08
	449281	AJ808689	Hs.182717	NM_030766:Homo sapiens hypothetical prot	4.08
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	4.08
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
	435066	BE261750	Hs.4747	NM_001363:Homo sapiens dyskeratosis cong	4.05
10	414753	AF158255	Hs.77225	NM_008437:Homo sapiens ADP-ribosyltransf	4.04
	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of lu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.03
	431657	AJ345227	Hs.105448	Hs.105448:protein kinase, lysine defic	4.01
15	439759	AL368065	Hs.67709	Hs.67709:Homo sapiens mRNA full length i	4.00
	441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
	417800	BE250127	Hs.82906	Hs.82906:CDCC2 cell division cycle 20 ho	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
	456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
20	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGC14141	3.99
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	439437	U20536	Hs.3280	NM_001228:Homo sapiens caspase 6, apopto	3.97
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
25	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.96
	415000	AW026529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	3.94
30	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fis	3.94
	412610	X98088	Hs.74126	NM_001445:Homo sapiens fatty acid bindi	3.94
	433323	AA805132	Hs.159142	Hs.159142:juncal fringe homolog (Drosop	3.94
	422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
35	418113	AT217411	Hs.83484	Hs.83484:SRV (sex determining region Y)-	3.91
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE; 4341	3.89
	453439	AF572438	Hs.32976	NM_004486:Homo sapiens guanine nucleotid	3.89
	441888	AI733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
40	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
	425234	AW152225	Hs.165809	Hs.165809:ESTs. Weakly similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D131382	Hs.633325	NM_019894:Homo sapiens transmembrane pro	3.85
	436251	BE515085	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	3.85
45	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in ml	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
	430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130888	Hs.58346	NM_022362:Homo sapiens ectodysplasin 1	3.82
	436481	AA379697	Hs.5199	NM_014178:Homo sapiens HSPC150 protein s	3.82
	453700	AB009426	Hs.560	NM_001644:Homo sapiens apolipoprotein B	3.81
	410819	BE512730	Hs.055114	Hs.055114:kazretin 18	3.81
55	409420	Z15008	Hs.54451	NM_005662:Homo sapiens laminin, gamma 2	3.79
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
	423179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (FJPHB3), mR	3.78

5	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin 1A (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis	3.64
	412140	AA219691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting	3.64
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs.2316:SRF (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
10	412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401519				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prolid	3.58
15	413936	AF113678	Hs.297681	NM_000295:Homo sapiens serine (or cyste	3.58
	424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
	431563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
	435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	AI650363	Hs.116462	Hs.116462:ESTs	3.57
20	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
	447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to puleoiv	3.56
	422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450863	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.56
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
	422532	AI008726	Hs.118126	(locuslink)NM_000308:Homo sapiens protea	3.55
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
30	437388	W52452	Hs.356768	Hs.356768:Homo sapiens mRNA; cDNA DKFZp7	3.54
	416927	AI120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020544	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, l	3.53
	432378	AI493046	Hs.146133	Hs.146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
35	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	3.51
	414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
	440340	AW896503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
	418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis	3.51
40	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kn	3.51
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	408231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.50
	453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC:24665	3.50
45	442700	AA377818	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
	410237	AI760589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442823	AW248322	Hs.95835		3.49
50	431648	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	3.48
	448993	AI471630	Hs.356952	Hs.356952:ESTs, Weakly similar to 090320	3.48
	447320	AI875419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	3.48
	414108	AI287592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
55	420996	AK001927	Hs.100895	(locuslink)NM_018089:Homo sapiens hypoth	3.47
	439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
	422158	L10343	Hs.112341	NM_002538:Homo sapiens protease inhibito	3.46
	418256	AW846318	Hs.12271	(locuslink)NM_012152:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_008713:Homo sapiens activated RNA pol	3.46
60	408709	AI355781	Hs.242463	Hs.242463:keratin 8	3.46
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AI080121	Hs.105460	NM_015393:Homo sapiens DKFZP584C00823 pro	3.45
	415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
	405451				3.44
65	414361	AI088138	Hs.204044	Hs.204044:ESTs	3.44
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417578	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.44
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25-dihydroxyvitami	3.43
	450883	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
70	421828	AW891865	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.42
	418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
	417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
75	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437675	AW854355	Hs.36829	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278811	NM_004482:Homo sapiens UDP-N-acetyl-alph	3.40
	439855	AW203959	Hs.149532	Hs.149532:ESTs	3.40
80	443891	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	3.40
	435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413818	N49813	Hs.75815	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424966	AF006005	Hs.154104	NM_002657:Homo sapiens pleiomorphic aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.37
5	427528	AU077143	Hs.178565	NM_002388:Homo sapiens MCM3 minichromosome	3.37
	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epitha	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018655:Homo sapiens anillin, actin bl	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
10	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	436746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	3.34
	456946	T29678	Hs.165068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:galanin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	3.33
20	416782	L35035	Hs.75886	(locuslink)NM_144563:Homo sapiens ribose	3.33
	426761	AI015709	Hs.172089	Hs.172089:pro-oncogene receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (gran	3.31
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	3.31
25	431192	AI670056	Hs.137274	Hs.137274:ESTs, Weakly similar to hypoth	3.30
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fi	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017695:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
30	410850	AW352867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.29
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403361				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
35	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
	452289	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443182	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.346183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-I	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
45	444371	BE640274	Hs.239	Hs.239:forkhead box M1	3.27
	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens stathmin 1 (lys	3.27
	403486				3.27
50	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
	421943	BE515520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-IRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T8937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949369	Hs.143600	Hs.143600:glutl phosphoprotein 4	3.24
60	435014	BE560898	Hs.10028	NM_022061:Homo sapiens ribosomal protein	3.24
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fi	3.24
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176658	NM_001189:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321679	NM_021085:Homo sapiens solute carrier fa	3.23
65	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
	408868	AW292286	Hs.255068	Hs.255068:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW138551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fi	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 fi	3.22
70	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457405	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
75	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	3.21
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	3.20
	444261	AA298968	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box H89 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
80	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155580	NM_001746:Homo sapiens calnexin (CANX)	3.19
	422283	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synth	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017836:Homo sapiens trans	3.18

5	419239	AA468183	Hs.335798	(locuslink)NM_033103:Homo sapiens rhophl	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (3.18
	425743	BE396495	Hs.169428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyl-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015869:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426058	AF038007	Hs.166196	NM_006603:Homo sapiens ATPase, Class I,	3.16
	416984	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	A1282759		AI282759:qt64a01.x1 NCL CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
15	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuv	3.15
	446595	T57448	Hs.15487	NM_017943:Homo sapiens hypothetical prot	3.15
20	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:coxsaackie virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.15
	438391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
25	409142	AL136577	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445673	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018948:Homo sapiens N-acetylneuramini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.14
	417791	AW965339	Hs.44289	Hs.44289:Homo sapiens cDNA FLJ37972 fis,	3.14
30	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	455906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-B-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannositas	3.13
35	409056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
	446386	A1032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50984	(locuslink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	M86899	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.10
45	434881	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27495	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
55	447760	AH31328	Hs.348605	NM_052953:Homo sapiens mitochondrial top	3.08
	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410168	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
60	442013	AA508476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	3.08
	431722	AF181528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421505	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439482	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to T06291	3.07
65	417866	AW967903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412530	AA768268	Hs.265273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW961952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_032659	Hs.179567	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW138099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25688 fis	3.05
	431945	AW000827	Hs.11982	NM_030768:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locuslink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
	403739				3.04
75	444864	N26362	Hs.11615	NM_016088:Homo sapiens map kinase phosph	3.04
	409152	AA176586	Hs.194346	Hs.194346:Spr-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
80	450553	AW860613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens sirtui	3.03
	440088	BE559877	Hs.183232	NM_024639:Homo sapiens hypothetical prot	3.02

	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
5	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
10	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (3.01
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens clepla	3.01
	417878	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2,5'-	3.01
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
	429883	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.00
15	417526	AA568908	Hs.82240	Hs.82240:syntaxin 3A	3.00
	414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
	409614	BE297412	Hs.55189	NM_016489:Homo sapiens 6'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
20	433312	AI241331	Hs.131766	Hs.131766:ESTs, Moderately similar to l3	2.99
	420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.96808	Hs.96808:hypothetical protein FLJ20485	2.99
25	413080	AW04232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	M71826	Hs.105485	NM_003095:Homo sapiens small nuclear rib	2.98
	439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
30	457211	AW872565	Hs.32399	(locuslink)NM_145240:Homo sapiens simila	2.98
	410467	AF102548	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
	422066	AW249275	Hs.343521	Hs.343521:malic dehydrogenase 2, NAD (m	2.97
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
35	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M95956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	2.97
	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
	417911	AA333387	Hs.82916	Hs.82918:chaperonin containing TCP1, sub	2.96
40	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.96
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
	418245	AA088767	Hs.63883	NM_020162:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
45	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
	439559	AW870780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
50	432843	BE250865	Hs.279529	NM_013237:Homo sapiens px19-like protein	2.95
	406684	X16354	Hs.50884	(locuslink)NM_001712:Homo sapiens carcin	2.95
	410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transl	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
55	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906897	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
	446696	AF279265	Hs.298478	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.89859	(locuslink)NM_004911:Homo sapiens protei	2.93
60	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.93
	428376	AF119565	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
65	428048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	426378	U80082	Hs.169500	Hs.169500:KIAA0826 protein	2.92
	422397	AJ223368	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
70	443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	2.92
	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_008420	Hs.118249	Hs.118249:ADP-ribosylation factor guenin	2.92
75	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
	429628	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278954	NM_007276:Homo sapiens chromobox homolog	2.92
	400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
80	419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guenin	2.91
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE395290	Hs.5097	Hs.5097:synaptobrevin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

	433487	U31814	Hs.3352	NM_001527: Homo sapiens histone deacetylase	2.91
	416933	BE581850	Hs.80506	NM_003090: Homo sapiens small nuclear rib	2.90
	430287	AW182459	Hs.125759	Hs.125759: likely ortholog of mouse RING	2.90
5	434026	R15486	Hs.285218	(locuslink)NM_021213: Homo sapiens phosph	2.90
	447698	AJ420156	Hs.326733	NM_052858: Homo sapiens similar to RIKEN	2.90
	411263	BE297802	Hs.69360	NM_006845: Homo sapiens kinesin-like 6 (m	2.90
	432754	BE241691	Hs.3100	Hs.3100: lysyl-tRNA synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398: guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046: Homo sapiens exosomal core pro	2.90
	420421	AF281133	Hs.343589	Hs.343589: axosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062: chromosome 20 open reading fra	2.89
	414420	AA043424	Hs.76095	NM_052815: Homo sapiens immediate early r	2.89
	457284	AF102850	Hs.227933	NM_013338: Homo sapiens Alg5, S. cerevisi	2.89
15	401405				2.89
	453111	AB014598	Hs.31720	NM_014799: Homo sapiens hephaestin (HEPH)	2.89
	400247		Hs.358473	NM_006713: Homo sapiens activated RNA pol	2.89
	421910	NM_014586	Hs.109437	NM_014586: Homo sapiens hormonally upregu	2.89
	413610	AL117554	Hs.119808	NM_015934: Homo sapiens nucleolar protein	2.89
20	413588	AA971014	Hs.75432	NM_008864: Homo sapiens IMP (inosine mono	2.89
	418651	NM_001949	Hs.1189	NM_001949: Homo sapiens E2F transcription	2.88
	427490	Z95152	Hs.178895	NM_002754: Homo sapiens mitogen-activated	2.88
	417634	W27202	Hs.82327	NM_000178: Homo sapiens glutathione synth	2.88
	435099	AC004770	Hs.4756	NM_004111: Homo sapiens flap structure-sp	2.88
25	425811	AL039104	Hs.159557	NM_002266: Homo sapiens karyopherin alpha	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207: Homo sapiens cleava	2.88
	412974	R18978	Hs.75105	NM_006579: Homo sapiens emopamil binding	2.88
	413179	N99692	Hs.75227	NM_005002: Homo sapiens NADH dehydrogenas	2.88
	407770	AW607831	Hs.38738	NM_014343: Homo sapiens claudin 15 (CLDN1	2.88
30	408847	AW290997	Hs.190153	Hs.190153: Homo sapiens cDNA FLJ33988 fis	2.87
	448250	NM_016034	Hs.20776	(locuslink)NM_016034: Homo sapiens mitoch	2.87
	428810	AF068238	Hs.193788	NM_006625: Homo sapiens nitric oxide synt	2.87
	427505	AA361562	Hs.178761	Hs.178761: 26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146: v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894: ESTs, Highly similar to S02392	2.87
	409282	AK000631	Hs.52256	Hs.52256: hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222: estrogen receptor binding site a	2.87
	460378	AW249181	Hs.154796	Hs.154796: Homo sapiens cDNA FLJ37876 fis	2.86
	411761	AI733848	Hs.71935	NM_021220: Homo sapiens zinc finger prote	2.86
40	415681	AW963979	Hs.24723	Hs.24723: ESTs	2.86
	417716	AW969587	Hs.86366	Hs.86366: ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931: hypothetical protein FLJ10607 s	2.86
	436138	H53323	Hs.25717	Hs.25717: Homo sapiens cDNA: FLJ23454 fis	2.86
	432858	BE818609	Hs.279591	Hs.279591: Homo sapiens, Similar to RNA p	2.86
45	434457	AF141332	Hs.200333	NM_018680: Homo sapiens apolipoprotein B4	2.86
	444237	AA336878	Hs.9842	Hs.9842: ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831: Homo sapiens nuclea	2.85
	411393	AW797437	Hs.69771	NM_001710: Homo sapiens B-factor, proper	2.85
	424270	AK001818	Hs.144407	NM_018283: Homo sapiens hypothetical prot	2.85
50	414396	BE548266	Hs.76057	(locuslink)NM_000403: Homo sapiens galact	2.85
	426120	AA325243	Hs.166887	Hs.166887: copine 1	2.85
	446663	BE614599	Hs.356501	(locuslink)NM_032335: Homo sapiens hypo	2.85
	443802	AW504924	Hs.9805	Hs.9805: exportin 5	2.85
	445863	R12234	Hs.13396	Hs.13396: Homo sapiens clone 25028 mRNA s	2.85
55	434808	AF155108	Hs.258150	Hs.258150: NY-REN-41 antigen	2.85
	440334	BE275112	Hs.7165	NM_003904: Homo sapiens zinc finger prote	2.85
	449057	AB037784	Hs.22941	Hs.22941: KIAA1363 protein	2.85
	432680	T47384	Hs.278613	(locuslink)NM_005532: Homo sapiens interf	2.84
60	446421	BE297434	Hs.15071	Hs.15071: chaperonin containing TCP1, sub	2.84
	427239	BE270447	Hs.356512	Hs.356512: ESTs, Weakly similar to UBCA_	2.84
	425849	U30930	Hs.158540	(locuslink)NM_003350: Homo sapiens UDP gl	2.84
	429638	AJ916652	Hs.211577	(locuslink)NM_004956: Homo sapiens kinect	2.84
	435777	AW419202	Hs.286192	NM_032182: Homo sapiens protein phosphat	2.84
	424441	X14850	Hs.147097	Hs.147097: H2A histone family, member X	2.84
65	407833	AW955632	Hs.86666	Hs.86666: chromosome 7 open reading frame	2.84
	415083	AI632683	Hs.27179	Hs.27179: Homo sapiens cDNA FLJ12933 fis	2.83
	421482	AF016495	Hs.104624	NM_020680: Homo sapiens aquaporin 9 (AQP9	2.83
	443572	AA025610	Hs.9605	Hs.9605: cleavage and polyadenylation spe	2.83
	443180	R15875	Hs.258576	NM_012129: Homo sapiens claudin 12 (CLDN1	2.83
70	413753	U17760	Hs.75517	NM_000228: Homo sapiens laminin, beta 3 (2.83
	453028	AB006532	Hs.31442	NM_004260: Homo sapiens RecQ protein-like	2.83
	425047	U34038	Hs.154299	NM_005242: Homo sapiens coagulation facto	2.83
	432593	AW301003	Hs.51483	Hs.51483: Homo sapiens, Similar to RIKEN	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_005518: Homo sapiens 3-hydr	2.83
75	413095	AA494359	Hs.30715	Hs.30715: potassium voltage-gated channel	2.83
	417677	NM_016055	Hs.82389	NM_016055: Homo sapiens mitochondrial rib	2.83
	425263	NM_001197	Hs.165419	NM_001197: Homo sapiens BCL2-interacting	2.82
	437430	W44671	Hs.124	NM_014628: Homo sapiens gene predicted fr	2.82
	428289	M26301	Hs.2253	Hs.2253: complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193518	NM_003921: Homo sapiens B-cell CLL/lympho	2.82
	432633	AI796390	Hs.210667	Hs.210667: ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575: ESTs	2.82

5	410045	AA808930	Hs.58189	Hs.58189:eukaryotic translation initiat	2.82
	454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
	434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
10	428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
	416047	BE439894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
	452199	BE255543	Hs.110895	Hs.110895:hypothetical protein MGC3133	2.81
	425998	ALJ076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
15	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
	436127	W94824	Hs.11585	NM_080748:Homo sapiens chromosome 20 ope	2.80
	418731	AL264688	Hs.11197	NM_002157:Homo sapiens heat shock 10kD p	2.80
20	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associ	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
	409463	AI458165	Hs.17256	NM_023930:Homo sapiens hypothetical prot	2.79
	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
25	416960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
	434750	BE019254	Hs.4112	Hs.4112:t-complex 1	2.79
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
30	400529				2.79
	436414	BE264633	Hs.143638	NM_033681:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
	427953	AI042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (2.79
	426459	AF151812	Hs.169892	NM_019366:Homo sapiens serologically def	2.79
35	413880	AI680842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
	442468	N77737	Hs.8349	NM_138933:Homo sapiens apobec-1 compleme	2.79
	413476	U26849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
	413278	BE563085	Hs.833	Hs.833:Interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putati	2.79
40	452075	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.81381	Hs.81381:heterogeneous nuclear ribonucle	2.79
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
	409836	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	2.78
	447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
45	434845	BE287057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE268042	Hs.9681	Hs.9681:proteasome (prosome, macropain)	2.78
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
	430512	AF182294	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associat	2.78
50	432638	AA340864	Hs.278582	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE268134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
	448083	AW877382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
55	443343	BE409808	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	416313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF028004	Hs.141860	NM_004366:Homo sapiens chloride channel	2.77
	458950	AF111170	Hs.308165	Hs.308165:ESTs, Highly similar to unknow	2.77
	432543	AA552890	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
60	423271	W47225	Hs.126256	NM_000578:Homo sapiens Interleukin 1, be	2.77
	410695	AW629223	Hs.64794	NM_006878:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
	457757	AA434108	Hs.12271	NM_012182:Homo sapiens F-box and leucine	2.77
	420186	NM_015925	Hs.95697	Hs.95697:diver-specific bHLH-Zip transcr	2.77
65	410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
	432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
	446658	AI440137	Hs.184989	NM_138492:Homo sapiens hypothetical prot	2.76
70	419465	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
	414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	406530	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
75	432320	AW411086	Hs.274351	NM_018032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
	433908	NM_014062	Hs.3568	Hs.3568:ART-4 protein	2.76
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
80	446946	AI878932	Hs.317	NM_003288:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
	433862	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
	417080	BE392846	Hs.1053	Hs.1053:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416188	BE157260	Hs.75070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

5	419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication initi	2.75
	407871	AI469117	Hs.62918	Hs.62918:CDK91 cell division cycle 91-B	2.75
	432403	AA550815	Hs.124840	(locuslink)NM_138456:Homo sapiens hypoth	2.75
	410775	AB014460	Hs.66196	NM_002528:Homo sapiens rth endonuclease	2.75
	444197	BE288947	Hs.10590	NM_018883:Homo sapiens zinc finger prota	2.75
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
10	433662	W07162	Hs.150828	NM_020387:Homo sapiens RAB25, member RAS	2.74
	428235	AE319564	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fis,	2.74
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_018094:Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	2.74
15	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
20	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens miRNA; cDNA DKFZp4	2.73
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_006869:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ53433 fis	2.73
25	452461	N78223	Hs.108108	Hs.108108:ubiquitin-like, containing PHD	2.73
	407699	AA825974	Hs.32546	NM_024622:Homo sapiens hypothetical prot	2.73
	412258	AA376768	Hs.98125	(locuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AI215948	Hs.143969	Hs.143969:ESTs	2.72
30	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone famil	2.72
	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
	424585	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	2.72
	424692	AA428834	Hs.151791	NM_014679:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014:Homo sapiens FK506 binding pro	2.72
35	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	2.72
	450164	AI239923	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.71
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ110901	2.71
	450897	W16741	Hs.351629	NM_014017:Homo sapiens HSPC003 protein (2.71
	447349	A375546	Hs.501577	BE743847:501577785F1 NIH_MGC_9 Homo sapi	2.71
40	445413	AA151342	Hs.12677	(locuslink)NM_016077:Homo sapiens CGI-14	2.71
	448826	AI580252	Hs.255565	Hs.255565:Homo sapiens cDNA FLJ33892 fis	2.71
	406671	AA125647	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatrin (EPB27)-like 2	2.71
	441020	W79293	Hs.35962	Hs.35962:Homo sapiens miRNA; cDNA DKFZp68	2.70
45	458933	AI638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439856	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW087800	Hs.155223	NM_003714:Homo sapiens stannocalcin 2 (2.70
50	420085	AI741809	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14182 fis,	2.70
	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW875531	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_016939:Homo sapiens CGI-09 protein (L	2.70
55	421344	AW631030	Hs.103865	(locuslink)NM_015873:Homo sapiens villin	2.70
	446607	AI601065	Hs.155780	Hs.155780:ESTs	2.70
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347:Homo sapiens papidyl protyl	2.70
	413794	AF294532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
60	451481	AA300228	Hs.295868	(locuslink)NM_030974:Homo sapiens hypoth	2.70
	458820	BE562151	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AA579405	Hs.8854	Hs.8854:Pvt1 oncogene homolog, MYC activ	2.69
65	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_022145:Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551:Homo sapiens intrunoglobulin (C	2.69
	422516	BE259862	Hs.117950	NM_006452:Homo sapiens phosphatidylamini	2.69
	416084	L16991	Hs.79008	NM_012145:Homo sapiens deoxythymidylate	2.69
70	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
	424373	AJ133798	Hs.146218	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	AA188809	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interleukin enhancer binding fa	2.69
75	420062	AW411096	Hs.84785	(locuslink)NM_021809:Homo sapiens YGFB-i	2.69
	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381:hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	2.68
80	421933	R88881	Hs.109655	NM_006746:Homo sapiens sex comb on midle	2.68
	417750	AI287720	Hs.260523	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425801	AW629485	Hs.140720	NM_012083:Homo sapiens frequently reara	2.68

5	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	2.68
	429344	R94038	Hs.374864	NM_005538:Homo sapiens inhibin, beta G (2.68
	427719	AI393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20889 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
10	413142	M81740	Hs.75212	(locuslink)NM_002539:Homo sapiens omith	2.67
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
15	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108909	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
20	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu ⁺⁺ tran	2.67
	445304	BE813206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.68
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AI869664	Hs.351863	(locuslink)NM_003312:Homo sapiens thioeu	2.66
25	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374073	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	2.66
	456248	AL035788	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427891	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
30	419705	AW368634	Hs.154331	Hs.154331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coat protein gamm	2.66
	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40389 fis	2.66
	446356	AB16736	Hs.14886	Hs.14886:zinc finger, DHH domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
35	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
	431127	U68618	Hs.250581	Hs.250581:SWI/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
40	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
	412738	N34731	Hs.74582	NM_078480:Homo sapiens fuse-binding prot	2.65
	409893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenanc	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP584I1171 protein	2.64
	428072	BE268602	Hs.182366	NM_016292:Homo sapiens heat shock protei	2.64
45	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	2.64
50	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
	406633	AW863372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (2.64
	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432984	AF118395	Hs.278865	NM_014317:Homo sapiens trans-prenyltrans	2.63
	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
55	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	AI694131	Hs.29002	Hs.28002:KIAA1706 protein	2.63
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37064	Hs.37054:ephrin-A3	2.63
	430024	AB088780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	2.63
60	406122				2.63
	420988	AW006352	Hs.158843	Hs.159643:ESTs, Weakly similar to putati	2.63
	436433	AW631437	Hs.6184	(locuslink)NM_016397:Homo sapiens TH1-li	2.63
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410387	AF217517	Hs.63042	NM_018467:Homo sapiens DKFZp564J157 prot	2.63
65	419420	AA365435	Hs.30724	(locuslink)NM_001516:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:cbx transmembrane epithelial an	2.63
	412599	AU076782	Hs.248287	(locuslink)NM_021128:Homo sapiens mercap	2.63
	436199	R38948	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.63
70	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CDAT1 protein (CD	2.62
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
	409703	NM_006187	Hs.56009	Hs.56008:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens Integral membrane	2.62
	418216	AA652240	Hs.283099	Hs.283099:AF15q14 protein	2.62
	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
75	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	2.62
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-28 protein (L	2.62
	429481	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
80	453335	AW857378	Hs.168238	NM_000149:Homo sapiens lucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens plecto	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	445766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

5	437033	AW248364	Hs.5409	(locuslink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC057 protein {	2.61
	414438	AI879277	Hs.76136	(locuslink)NM_003329:Homo sapiens thiora	2.61
	416221	BE513171	Hs.79086	(locuslink)NM_007208:Homo sapiens mltoc	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448825	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AI733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
15	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
	429770	AI766047	Hs.97736	Hs.99736:hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	430237	AI272144	Hs.236622	Hs.236522:DKFZP434P106 protein	2.60
	419607	RS2557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
	453258	AW293134	Hs.32597	NM_005877:Homo sapiens ring finger prote	2.60
	457234	AW968360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine {	2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
25	438533	AI40266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of Invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178578	(locuslink)NM_030677:Homo sapiens caleni	2.60
	463949	AU077146	Hs.35927	(locuslink)NM_006644:Homo sapiens heat s	2.59
30	451110	AI955040	Hs.285398	Hs.265398:ESTs, Moderately similar to hy	2.59
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.69877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	442990	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
35	424197	AF095834	Hs.142989	NM_015962:Homo sapiens germ cell specifi	2.59
	445680	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T88226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_008191:Homo sapiens proliferation-ass	2.59
40	441153	BE582826		BE582826:601336534F1 NIH_MGC_44 Homo sap	2.59
	410570	AH33098	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
45	449019	AI949095	Hs.67778	Hs.67778:Homo sapiens, clone IMAGE:54556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
50	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.288229	NM_012394:Homo sapiens profoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
55	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
	418803	U50079	Hs.88556	NM_004984:Homo sapiens histone deacetyl	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21768	Hs.21768:ESTs, Weakly similar to hypothe	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2f2 protein	2.57
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
60	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
	427254	AL121623	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001689:Homo sapiens arylsulfatase D {	2.57
	425689	W16489	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis	2.57
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427578	BE267756	Hs.180312	NM_016085:Homo sapiens mitochondrial rib	2.57
	444656	AI277924	Hs.145189	Hs.145189:ESTs, Weakly similar to hypothe	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
70	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
	409864	AW368228	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
75	418423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymer	2.56
	437623	D63860	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	2.56
80	418650	BE386750	Hs.88978	Hs.88978:prolyl endopeptidase	2.56
	425368	A2814595	Hs.155978	(locuslink)NM_003588:Homo sapiens cullin	2.56
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	2.56
	427878	AI494291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550964	Hs.89389	NM_005176:Homo sapiens ATP synthase, H+	2.56
	418432	BE391787	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.56

5	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ	2.55
	426410	BE298446	Hs.306890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	2.55
	402829				2.55
	425843	BE313280	Hs.156627	NM_004632:Homo sapiens death associated	2.55
	400895				2.55
10	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_018931:Homo sapiens tle485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.57898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
15	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	418681	AA287788	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
20	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
	446715	AJ337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KOEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003881:Homo sapiens pyridoxal (pyrido	2.54
25	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	456031	AA335896	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
30	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561810	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
	448775	AB025237	Hs.368	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_016956:Homo sapiens mitochondrial rib	2.53
35	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Humlin	2.53
40	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FL114076	2.53
	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
	426812	AF105355	Hs.172813	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA825401	Hs.122393	Hs.122393:ESTs	2.53
45	409289	AA046650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens perox	2.53
	412525	AA581439	Hs.152329	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.53
50	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation Initiat	2.53
	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155637	NM_008904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
55	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.53
	417691	AI076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-IIa 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI807114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	2.52
60	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_136391:Homo sapiens hypothetical prot	2.52
	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
65	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440687	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV688571	Hs.121066	(locuslink)NM_003270:Homo sapiens transm	2.52
70	424259	AK001778	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080548:Homo sapiens CDw82 antigen (CD	2.52
	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.52
75	433271	BE621697	Hs.14317	NM_018848:Homo sapiens nucleolar protein	2.51
	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exoninuc	2.51
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
80	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
	434474	AL042936	Hs.211571	(locuslink)NM_005333:Homo sapiens holoxy	2.51
	424482	BE288621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

5	421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIB	2.51
	435750	AB028012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
	452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alpha	2.51
	436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
	435877	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor Interac	2.51
	406363				2.51
10	452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
	421837	AI878857	Hs.109706	NM_016185:Homo sapiens hematological and	2.51
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
	434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
15	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
	426053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
	432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
	452390	AI854142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inact)	2.50
	400076				2.50
20	420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
	422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (Impo	2.50
	410723	AA100583	Hs.372108	Hs.372108:ESTs	2.50
	435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
25	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
	433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
	448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

30 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
	406885	0_0	M18728
	434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG899253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
40	432407	MH1429_12	BG036676 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE167999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856395 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986165 AK057283 BI861486 AA663341 AA457591 BG949284 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804864 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
45	406708	0_0	AJ282759
	453306	223120_4	AW578452
	447349	1063443_1	BE743847 AW809603 BM469626 AJ375546
50	441153	254480_3	BE862826 BE378727

TABLE 10C

55 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA --
 sequence of human chromosome 22" Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NT_position: Indicates nucleotide positions of predicted exons.

60	Pkey	Ref	Strand	NT_position
	404519	8152000	Plus	12817-13000
	406399	9258288	Minus	63448-63554
	403220	7630989	Plus	64338-64517
65	404661	9797073	Plus	33374-33675,33759-34008
	402498	9797769	Minus	8615-9103
	403055	8748904	Minus	109532-110225
	400965	7770576	Minus	173043-173564
70	403218	7630969	Plus	58039-58149
	401866	8018106	Plus	73126-73623
	403221	7630969	Plus	66294-66438,66936-67124
	401519	6649315	Plus	157315-157950
	405451	7622517	Minus	145949-146227
75	403532	8076842	Minus	81750-81901
	402944	9368423	Plus	110411-110716,111173-111640
	403219	7630969	Plus	61859-61995
	403381	9438267	Minus	26009-28178
	403485	9866528	Plus	2888-3001,3198-3532,3655-4117
80	405484	5922025	Plus	199214-199579,199572-199920,200262-20049
	404684	9797403	Minus	110881-111020
	402474	7547175	Minus	53526-53628,56765-55920,57530-57757
	405506	6466489	Plus	80014-80401,80593-81125
	403739	7630882	Plus	44563-44766,48209-48483,52265-52495

5	406545	7711510	Plus	145662-145781,147854-147984,148098-14824
	401405	7768126	Minus	69276-69452,69548-69958
	400750	8118067	Plus	198991-199168,199318-199548
	401179	9438647	Plus	113477-113883
	400529	9796988	Plus	138232-138423
	403817	8962065	Plus	110297-111052
	400446	9887687	Minus	177372-177674
	406122	9144087	Minus	30940-31386
10	406180	7283201	Minus	38923-39107
	402829	8918414	Plus	101532-101852,102005-102263
	400995	8098094	Plus	141186-141601
	404826	6572184	Plus	47726-48046
15	406363	9256114	Plus	14403-14602,17000-17147,17241-17368

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

30	Pkey:	Unique Eos probe set identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of tumor to normal adult tissues		
35	Pkey	ExAccn	UnigeneID	Unigene Title
	436749	AA684890	Hs.5302	NM_006149:Homo sapiens lectin, galactosyl
	406690	M29540	Hs.220529	(locuslink)NM_004383:Homo sapiens carcin
	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin
40	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,
	408667	M12523		
	437835	AW839591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intesti
45	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating iso
	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo
50	441031	AI110884	Hs.7645	NM_006141:Homo sapiens fibrinogen, B bet
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens tumor factor 1
	407243	AA058357	Hs.74486	(locuslink)NM_006890:Homo sapiens carcin
	422260	AA316993	Hs.105484	NM_032044:Homo sapiens regenerating gene
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)
55	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, Li c
	463863	X02544	Hs.572	Hs.572:homomorphid 1
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c
	436217	T63925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1
60	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21
	409153	W03754	Hs.50813	NM_017625:Homo sapiens Inteleclin (ITLN)
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque
	406399			
65	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob
	421984	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR
	423673	BE003054	Hs.1685	NM_002426:Homo sapiens matrix metallopro
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot
70	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso
	427583	M82952	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro
	406741	AA058357	Hs.74486	(locuslink)NM_006890:Homo sapiens carcin
	422424	AI186431	Hs.298638	Hs.298638:prostate differentiation facto
	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa
75	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr
	430569	AF241254	Hs.178098	NM_021894:Homo sapiens angiotensin I con
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc
80	428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),
	413585	AI133462	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma
	422664	AA316993	Hs.120879	Hs.120879:Homo sapiens, clone MGC:22871
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I

5	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protel	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homel	8.47
	452584	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfat	8.47
10	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	8.43
	421907	BE018558	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	8.12
	435538	AB011540	Hs.48930	Hs.4930:low density lipoprotein receptor	8.09
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
15	443426	AF088158	Hs.93329	(locuslink)NM_012112:Homo sapiens chromo	7.92
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
	408632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	7.71
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237058	Hs.237658:apolipoprotein A-II	7.48
20	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (Iscf	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451817	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
25	410418	D31382	Hs.63325	NM_018894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004818:Homo sapiens transmembrane 4 s	7.12
	414617	AK39520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	7.10
	447342	AF199288	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
	452194	AF64413	Hs.373999	Hs.373599:EST	7.02
30	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.96
35	415992	C06837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
	414798	AJ286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
	416214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411975	AI916068	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
40	408893	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
	428970	BE276891	Hs.194891	NM_003979:Homo sapiens retinoic acid ind	6.59
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	AJ345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	6.54
45	431330	X68532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	6.50
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056836	Hs.5366	NM_139063:Homo sapiens epidermal growth	6.45
50	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U67068	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, ba	6.19
55	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p80, CD71	6.18
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X76208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
60	426174	AA547969	Hs.115838	Hs.115838:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	409453	AI685516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000876	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	6.03
65	444161	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
	421408	AI688223	Hs.91096	NM_062816:Homo sapiens tripartite motif	5.95
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.92
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
70	428874	W32133	Hs.194388	Hs.194388:transferrin (prealbumin, amy	5.88
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.88
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
75	421379	Y15221	Hs.103982	NM_005408:Homo sapiens small inducible c	5.76
	433083	AL042769	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
	403218				5.74
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
80	429345	R11141	Hs.199895	Hs.199895:hypothetical protein MAC30	5.72
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425208	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

5	408889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW576849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	436746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
10	414590	NM_000508	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	5.56
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
	418508	AW997938	Hs.90786	NM_008786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	436251	BE515065	Hs.295535	(locuslink)NM_005392:Homo sapiens nucleo	5.41
20	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading tra	5.36
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
	422535	AA311914	Hs.164578	Hs.164578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288650	Hs.288650:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
25	430580	AW139724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AI493046	Hs.148133	Hs.148133:ESTs	5.25
	419593	AA133749	Hs.301350	Hs.301350:FXD domain-containing lon tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23856	5.21
30	415927	AL120166	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83768	NM_001827:Homo sapiens CDC28 protein kin	5.20
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446844	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
35	448051	BE048081	Hs.37054	Hs.37054:ephrin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	6.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
40	428478	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
	432575	AA553722	Hs.194346	Hs.194346:Spk-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
45	422609	Z46023	Hs.118721	NM_000434:Homo sapiens staldase 1 (tyso	5.06
	414361	AI086138	Hs.204044	Hs.204044:ESTs	5.04
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	436849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
50	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406673	M34996	Hs.198263	Hs.198263:major histocompatibility compl	4.99
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288827	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
55	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.98
	431548	AI834273	Hs.9711	NM_017615:Homo sapiens novel protein (HS	4.97
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014781	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M88849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
60	437009	AF127028	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
65	414108	AI287592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW180902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
70	408162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	4.87
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.87
	405484				4.87
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
75	428953	AA306610	Hs.348183	NM_003523:Homo sapiens tumor necrosis fa	4.86
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
80	417115	AW852782	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	426761	AD15709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R38762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKF2p4	4.77
	452721	AJ259529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

5	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50954	(locuslink)NM_001712:Homo sapiens carc	4.75
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	447965	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	4.72
	439863	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405566				4.70
10	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA316805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
15	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
	403739				4.61
	427490	Z95152	Hs.178895	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
20	424825	AF207059	Hs.163357	NM_001084:Homo sapiens procollagen-lysyl	4.60
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414895	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
25	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006846:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:cepha-AA	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
30	417578	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
	432407	AA221036		AF134184:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK5 protein tyro	4.53
	403219				4.53
35	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456905	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomuta	4.51
40	425743	BE396485	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50954	(locuslink)NM_001712:Homo sapiens carc	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.49
	426395	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
45	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	4.47
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422618	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355653	Hs.355653:ESTs	4.46
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
50	452888	AW956454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	4.46
	442013	AA508476	Hs.376009	Hs.376009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fls,	4.44
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
55	419559	Y07828	Hs.91086	NM_007028:Homo sapiens tripartite motif	4.44
	425880	L28339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	406847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fia	4.43
	431836	AF170532	Hs.271411	NM_138982:Homo sapiens beta-site APP-cle	4.43
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
60	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matric prot	4.41
	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432583	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421976	AW961017	Hs.6469	(locuslink)NM_024531:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
65	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422293	X04453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	4.38
	425998	AJ076829	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	4.37
	453111	AB014508	Hs.31720	NM_014790:Homo sapiens hapheslin (HEPH)	4.36
70	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	4.36
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166456	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.34
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte anti	4.34
75	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240: syntaxin 3A	4.32
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
80	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fls	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	429638	AI916882	Hs.211577	(locuslink)NM_004986:Homo sapiens kines	4.29

5	432636	AA340864	Hs.278562	NM_001307: Homo sapiens claudin 7 (CLDN7)	4.29
	412669	AA290712	Hs.82407	Hs.82407: chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.8661	Hs.8661: proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182: Homo sapiens transmembrane, pr	4.27
	409636	AA305729	Hs.18272	(focalink)NM_030674: Homo sapiens sokute	4.27
	408989	AW361666	Hs.49500	Hs.49500: KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530: Homo sapiens cDNA: FLJ23602 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126: Homo sapiens cDNA: FLJ22667 fi	4.24
10	431685	AW296135	Hs.267659	NM_006113: Homo sapiens vav 3 oncogene (v	4.24
	409956	AW103364	Hs.727	NM_002192: Homo sapiens inhibin, beta A (4.24
	413278	BE583085	Hs.833	Hs.833: Interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770: KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(focalink)NM_144624: Homo sapiens kinase	4.23
15	456629	AW891965	Hs.367942	Hs.367942: Homo sapiens, clone IMAGE:4701	4.23
	426682	AV680038	Hs.2056	Hs.2056: UDP glycosyltransferase 1 family	4.23
	418054	NM_002318	Hs.83354	NM_002318: Homo sapiens lysyl oxidase-like	4.22
	418626	BE019020	Hs.85838	NM_004207: Homo sapiens solute carrier fa	4.22
	437897	AA770551	Hs.146170	Hs.146170: hypothetical protein FLJ22969	4.21
20	435099	AC004770	Hs.4756	NM_004111: Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078	Hs.90078: nucleotide-sugar transporter sl	4.21
	421585	U95626	Hs.302043	NM_003965: Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147: Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840: TTK protein kinase	4.19
25	425283	NM_001197	Hs.155419	NM_001197: Homo sapiens BCL2-interacting	4.19
	426031	AA295251	Hs.166066	(focalink)NM_006697: Homo sapiens dspla	4.19
	441085	AW136551	Hs.181245	Hs.181245: Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75089	Hs.75089: serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246: Homo sapiens lymphocyte antigen	4.17
30	431842	NM_005764	Hs.271473	Hs.271473: epithelial protein up-regulate	4.17
	430367	AW372884	Hs.240770	Hs.240770: nuclear cap binding protein su	4.17
	404826				4.17
	414198	AW505308	Hs.75812	NM_004563: Homo sapiens phosphoenolpyruva	4.17
35	434203	BE262677	Hs.283558	NM_018509: Homo sapiens hypothetical prot	4.17
	426378	U80082	Hs.169600	Hs.169600: KIAA0826 protein	4.16
	433020	AI375726	Hs.227152	NM_016391: Homo sapiens hypothetical prot	4.16
	420319	AW406289	Hs.96593	NM_019034: Homo sapiens ras homolog gene	4.15
	446696	AF279265	Hs.298476	NM_022911: Homo sapiens solute carrier fa	4.15
	400130		Hs.155660	NM_001746: Homo sapiens calnexin (CANX),	4.14
40	431890	X17033	Hs.271986	NM_002203: Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149	NM_014481: Homo sapiens APEX nuclease (ap	4.13
	417396	AL037228	Hs.301957	NM_018144: Homo sapiens Sec61 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491: Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150276	Hs.150276: KIAA0241 protein	4.13
45	445462	AA378776	Hs.288649	(focalink)NM_024051: Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510	Hs.184510: stratiotin	4.12
	408012	AL117435	Hs.49725	Hs.49725: DKFZP434I216 protein	4.11
	424164	AF026004	Hs.141660	NM_004368: Homo sapiens chloride channel	4.10
	400290	H18836	Hs.31608	(focalink)NM_017636: Homo sapiens transi	4.10
50	409152	AA176585	Hs.194346	Hs.194346: Spir-2 protein	4.10
	427333	AF067797	Hs.176658	NM_001169: Homo sapiens aquaporin 8 (AQP8	4.10
	413835	AI272727	Hs.249183	NM_024306: Homo sapiens fatty acid hydrox	4.09
	444664	N26362	Hs.11615	NM_016086: Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622: Homo sapiens cytochrome P450,	4.09
55	407777	AA181071	Hs.71465	Hs.71465: squalene epoxidase	4.09
	414806	D14694	Hs.77329	(focalink)NM_014754: Homo sapiens phosph	4.08
	421190	U95031	Hs.102482	Hs.102482: mucin 6, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614: Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993: Homo sapiens nucleophosmin/nuc	4.06
60	414907	X90725	Hs.77597	NM_000898: Homo sapiens ribosomal protein	4.06
	425247	NM_005840	Hs.155324	Hs.155324: matrix metalloproteinase 11 (s	4.05
	443802	AW504924	Hs.9805	Hs.9805: ceroplatin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169: Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256150	Hs.256150: NY-REN-41 antigen	4.04
65	428376	AF119665	Hs.184011	Hs.184011: pyrophosphatase (inorganic)	4.04
	418216	AA682240	Hs.283099	Hs.283099: AF15q14 protein	4.02
	436278	BE396290	Hs.5097	Hs.5097: synaptophysin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586: Homo sapiens hormonally upregu	4.02
	417866	AW087903	Hs.82772	Hs.82772: collagen, type XI, alpha 1	4.02
70	449057	AB037784	Hs.22941	Hs.22941: KIAA1363 protein	4.01
	414581	AI084813	Hs.195155	Hs.195155: solute carrier family 38, memb	4.00
	414812	X72755	Hs.77367	NM_002416: Homo sapiens monokine induced	4.00
	456362	AW973003	Hs.179809	(focalink)NM_024831: Homo sapiens nuclea	3.99
	431958	X83629	Hs.28377	NM_001793: Homo sapiens cadherin 3, type	3.98
75	418661	NM_001949	Hs.1189	NM_001949: Homo sapiens E2F transcription	3.98
	419092	J05581	Hs.89603	NM_002458: Homo sapiens mucin 1, transmem	3.98
	414013	AA766805	Hs.47099	NM_024642: Homo sapiens hypothetical prot	3.98
	409093	BE243834	Hs.50441	NM_015936: Homo sapiens CGI-04 protein (L	3.97
	445873	AA250970	Hs.251946	Hs.251946: Homo sapiens cDNA FLJ11840 fis	3.96
80	436485	X59135	Hs.156110	Hs.156110: immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377	Hs.112377: cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398	Hs.5398: guanine monophosphate synthetase	3.94
	449437	AJ702038	Hs.100057	Hs.100057: serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286: Homo sapiens topoisomerase (DN	3.94

5	420162	BE378432	Hs.95577	NM_052984: Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129: Homo sapiens claudin 12 (CLDN1	3.93
	418736	AW388633	Hs.6682	Hs.6682: solute carrier family 7, (cation	3.93
	409463	AA58165	Hs.17296	NM_023930: Homo sapiens hypothetical prot	3.92
	447495	AW401864	Hs.18720	NM_004208: Homo sapiens programmed cell d	3.92
	448093	AW977382	Hs.15898	Hs.15898: 2,4-dienoyl CoA reductase 2, pe	3.91
	428698	AA852773	Hs.334838	Hs.334838: KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718: Homo sapiens cDNA FLJ33433 fis	3.89
10	435827	H72187	Hs.356668	(locuslink)NM_005274: Homo sapiens guanine	3.89
	407971	AA69117	Hs.62918	Hs.62918: CDC91 cell division cycle 91-1	3.89
	400750				3.89
	448140	AF146761	Hs.20450	NM_020125: Homo sapiens B lymphocyte acti	3.89
	413680	AI680842	Hs.110915	NM_021258: Homo sapiens interleukin 22 re	3.89
15	453258	AW293134	Hs.32597	NM_005977: Homo sapiens ring finger prote	3.89
	428788	AF082283	Hs.193516	NM_003921: Homo sapiens B-cell CLL/lympho	3.88
	443044	N28522	Hs.8935	NM_014298: Homo sapiens quinoximate phosph	3.88
	413095	AA494359	Hs.30715	Hs.30715: potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684: calcitonin gene-related peptid	3.87
20	410268	AA316181	Hs.81635	NM_012449: Homo sapiens six transmembrane	3.87
	425047	U34038	Hs.154299	NM_005242: Homo sapiens coagulation facto	3.87
	416084	L16991	Hs.79006	NM_012145: Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860: KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635: six transmembrane epithelial an	3.85
25	407770	AW607631	Hs.38738	NM_014343: Homo sapiens claudin 15 (CLDN1	3.85
	418313	BE244231	Hs.84038	NM_015937: Homo sapiens CGI-06 protein (L	3.85
	413380	AI904232	Hs.75323	Hs.75323: prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296: ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884: Homo sapiens IMP (inosine mono	3.85
30	433658	L03678	Hs.156110	Hs.156110: immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523: serine/threonine kinase 38 lik	3.84
	430237	AI272144	Hs.236522	Hs.236522: DKFZP434P106 protein	3.84
	414862	BE521310	Hs.923	Hs.923: single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.6947	NM_005370: Homo sapiens met transforming	3.84
35	427318	AF186081	Hs.175783	NM_014578: Homo sapiens solute carrier fa	3.83
	459306	AW578452		AW578452: RC1-CT0252-030100-023-b07 CT025	3.83
	446342	BE298665	Hs.14846	Hs.14846: Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704: chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321: WD repeat domain 18	3.82
40	428514	BE616633	Hs.170195	Hs.170195: bone morphogenetic protein 7 (3.82
	410315	AI638871	Hs.378965	Hs.378965: Homo sapiens cDNA FLJ37658 fis	3.82
	421905	AK60247	Hs.32699	Hs.32699: Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696: KIAA1324 protein	3.81
	445921	AW016211	Hs.153799	Hs.153799: Homo sapiens cDNA FLJ38333 fis	3.80
45	414368	W70171	Hs.75939	NM_012474: Homo sapiens uridine monophosp	3.80
	457284	AF102850	Hs.227833	NM_013338: Homo sapiens Alg5, S. cerevisi	3.80
	413813	M86956	Hs.75551	NM_003212: Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886: Homo sapiens mal, T-cell diffe	3.80
	410219	T98228	Hs.171952	Hs.171952: occludin	3.80
50	407137	T97307			3.78
	430462	AI584156	Hs.105640	Hs.105640: hypothetical protein BC007772	3.78
	432880	T47384	Hs.278613	(locuslink)NM_005532: Homo sapiens interf	3.78
	450010	AW293801	Hs.255052	Hs.255052: ESTs	3.78
	440334	BE276112	Hs.7165	NM_003904: Homo sapiens zinc finger prote	3.78
55	440878	NM_004987	Hs.112378	(locuslink)NM_004987: Homo sapiens LIM an	3.77
	428072	BE258602	Hs.182366	NM_016292: Homo sapiens heat shock protei	3.77
	407722	BE252241	Hs.38041	NM_003681: Homo sapiens pyridoxal (pyrido	3.77
	428459	AF151812	Hs.168992	NM_015966: Homo sapiens serologically def	3.77
	443323	BE660621	Hs.9222	Hs.9222: estrogen receptor binding site a	3.76
60	406621	X57809	Hs.181125	Hs.181125: immunoglobulin lambda locus	3.76
	423198	M81933	Hs.1634	Hs.1634: cell division cycle 25A	3.76
	428205	AB020643	Hs.183006	Hs.183006: likely homolog of mouse hepari	3.75
	447200	BE543148	Hs.281434	Hs.281434: Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895: Homo sapiens casein kinase 2,	3.74
65	411950	T28407	Hs.81664	NM_002619: Homo sapiens platelet factor 4	3.74
	418681	AA287785	Hs.23449	Hs.23449: insulin receptor tyrosine kinas	3.74
	421532	AW138207	Hs.146170	NM_022842: Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623: interferon, gamma-inducible pro	3.74
	435886	BE255839	Hs.12126	NM_018487: Homo sapiens hepatocellular ca	3.73
70	417288	AA122237	Hs.81874	NM_002413: Homo sapiens microsomal glutat	3.73
	421743	T35958	Hs.107614	Hs.107614: DKFZP564I1171 protein	3.73
	400419	AF084646		AF084646: Homo sapiens versican Vint isofo	3.73
	421357	AK000809	Hs.103808	NM_017896: Homo sapiens chromosome 20 ope	3.73
	420665	AW468240	Hs.371581	Hs.371581: ESTs	3.73
75	418703	NM_014448	Hs.87435	Hs.87435: Rho guanine exchange factor (GE	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182: Homo sapiens transm	3.72
	419743	AW408762	Hs.5957	Hs.5957: Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020636	Hs.4984	Hs.4984: KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795: lactate dehydrogenase A	3.72
80	444008	BE396085	Hs.334762	(locuslink)NM_032832: Homo sapiens hypoth	3.72
	442875	BE625003	Hs.23625	Hs.23625: Homo sapiens clone TCCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348: Homo sapiens ubiquitin-conjuga	3.71
	413950	AA249096	Hs.32793	Hs.32793: Homo sapiens cDNA FLJ31108 fis	3.71
	411125	AA151647	Hs.68877	Hs.68877: cytochrome b-245, alpha polypep	3.71

5	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.63563	NM_001853:Homo sapiens collagen, type IX	3.70
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
10	408846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AJ694131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
	413179	N99892	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
15	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076608	Hs.2934	NM_001033:Homo sapiens ribonucleotide re'	3.69
	413781	J06272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374684	NM_005538:Homo sapiens inhibin, beta C (3.69
	442315	AA173592	Hs.7956	Hs.7956:ESTs	3.68
20	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-rat strian leuk	3.66
25	409402	AF208234	Hs.695	Hs.695:scystein B (stefin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AJ796390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
30	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247830	NM_002991:Homo sapiens small inducible c	3.65
	432920	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA570265	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
35	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AJ807114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
	412948	BE243313	Hs.334851	Hs.334851:UIM and SH3 protein 1	3.62
	452098	AJ858183	Hs.79305	BF755039:QV0-CT0583-181000-428-107 CT058	3.62
40	430024	AJ808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
45	412841	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
	453331	AJ240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31068 fis	3.60
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
50	417389	BE260984	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.59
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AJ878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
	446556	AJ818738	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001660:Homo sapiens Interleukin 13 re	3.59
55	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420631	A1652069	Hs.98614	NM_004597:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
	447698	AJ420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
60	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, I	3.57
	452284	AJ077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:phosphatase domain containing 1	3.56
	434224	AA380731	Hs.84	NM_000208:Homo sapiens Interleukin 2 rec	3.56
	425322	U83630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
65	438407	AA571122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.56
	413859	AW992355	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, I	3.56
	427268	X78520	Hs.174139	NM_001828:Homo sapiens chloride channel	3.55
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ep	3.55
	411704	AJ499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
70	452700	AJ859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
	422813	AV856571	Hs.121088	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
75	432268	BE311856	Hs.274220	Hs.274220:3'-phosphoadenosine 5'-phospho	3.54
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
	421802	BE281458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
	428502	BE336599	Hs.185055	Hs.185055:BENE protein	3.53
80	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoza	3.53
	408716	AI587839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.52
	442007	AA301116	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421612	AF161254	Hs.106195	(locuslink)NM_016579:Homo sapiens B26 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

	428023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
	452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
	404240				3.50
5	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
10	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.49
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.49
15	439841	AF038961	Hs.8710	NM_004870:Homo sapiens mannose-P-dolicho	3.49
	428390	AK40377	Hs.350077	NM_000692:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	3.48
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE387202	Hs.118838	Hs.118838:non-malignant cells 1, protei	3.48
20	457635	AV680976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
	454390	AB020713	Hs.69966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	402829				3.47
	451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AJ741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA786142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
	439223	AW238299	Hs.250818	NM_025217:Homo sapiens UL18 binding prot	3.46
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW298454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AI359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	3.45
35	433627	AF078866	Hs.294296	NM_033161:Homo sapiens surfactant 4 (SURF4)	3.45
	400263		Hs.76309	NM_001951:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.45
	410838	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknown	3.44
40	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	Hs.326525	NM_001659:Homo sapiens arylsulfatase D {	3.44
45	425274	BE281181	Hs.155462	Hs.155462:MCM5 minichromosome maintenanc	3.44
	448913	AA194422	Hs.22584	NM_004998:Homo sapiens myosin VI (MYO6),	3.44
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	Hs.73863	NM_001200:Homo sapiens bone morphogenesi	3.43
	424482	BE286621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltage	3.43
50	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (protease)	3.43
	422386	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
	428093	AW584506	Hs.104830	Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.42
55	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
	427597	D16049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
	427648	AK376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.41
60	453802	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 op	3.41
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	3.41
	414045	NM_002951	Hs.76722	NM_002951:Homo sapiens ribophorin II (RP	3.41
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
	443303	U87319	Hs.8216	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
65	422256	ME4673	Hs.1499	NM_005528:Homo sapiens heat shock transc	3.40
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
	400205		Hs.81848	NM_006265:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363				3.39
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methyl	3.39
75	423309	BE006776	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119886	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
	400125		Hs.126078	(locuslink)NM_004162:Homo sapiens ornith	3.38
80	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	Hs.61980	NM_018992:Homo sapiens hypothetical prot	3.37
	434626	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI805684	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.37
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.37

5	446715	AJ337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426789	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
	406698	X03088	Hs.73931	Hs.73931:major histocompatibility comple	3.36
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.36
	418662	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA298741	Hs.102136	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30716:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.36
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholesta	3.36
	436415	BE285264	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.36
15	457329	AJ634860	Hs.359982	(locuslink)NM_016442:Homo sapiens type 1	3.35
	432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
	412525	AA581439	Hs.162328	Hs.162328:ESTs	3.35
	416391	AJ878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
20	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
	402652		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
	422598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
	450508	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
25	437295	AA350394	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.34
	439246	AI98072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
30	448775	AB025237	Hs.388	NM_002452:Homo sapiens nucleic (nucleoside	3.34
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locuslink)NM_017796:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
35	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ13360 fis	3.33
	415938	BE389507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.76871	(locuslink)NM_012408:Homo sapiens protei	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338905	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AI557486	Hs.171922	Hs.171922:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythrobl	3.32
	430393	BE185030	Hs.241305	(locuslink)NM_005470:Homo sapiens tripar	3.32
45	402104				3.32
	446620	AA128808	Hs.178902	(locuslink)NM_022109:Homo sapiens CDw92	3.32
	443425	AJ056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926980	Hs.346669	Hs.346669:CD22B protein kinase 1	3.31
50	413053	AL036737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
	451564	AJ078698	Hs.132780	(locuslink)NM_001467:Homo sapiens glucos	3.31
	437822	AW450485	Hs.4437	NM_000491:Homo sapiens ribosomal protein	3.31
	441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
55	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fis485 (LOC51066)	3.31
	448608	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytole	3.31
	448644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA156177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucose	3.31
60	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
65	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phos	3.29
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
	442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CG1-69 protein (L	3.29
70	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
	417691	AJ076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
	412926	AI879078	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
	427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
75	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
	449199	AI890122	Hs.196988	Hs.196988:ESTs	3.28
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytole	3.28
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	3.28
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
80	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.28
	402260				3.28
	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.28
	408267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
	426812	AF105365	Hs.172813	NM_006598:Homo sapiens solute carrier fa	3.27

5	428671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain)	3.27
	434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (importin al	3.27
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
	448752	AA593887	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
10	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	3.26
	440286	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoxa	3.26
	428520	BE545884	Hs.343568	Hs.343566:KIAA0251 protein	3.26
15	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26
	425965	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	3.25
	449944	AF290512	Hs.58215	(locuslink)NM_030461:Homo sapiens rhotek	3.25
20	424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
	426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
	420190	AB16208	Hs.95887	(locuslink)NM_024112:Homo sapiens chromo	3.25
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
	418216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
25	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
	410800	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
	435640	AF220053	Hs.54950	NM_018468:Homo sapiens uncharacterized h	3.23
30	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
	430250	NM_018929	Hs.283021	NM_018929:Homo sapiens chloride intracel	3.23
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
	432731	R31178	Hs.287820	Hs.287820:fibrinectin 1	3.23
35	410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
	430075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw82 antigen (CD	3.22
40	403912				3.22
	425782	NM_005754	Hs.220889	Hs.220889:Ras-GTPase-activating protein	3.22
	416178	AB085527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
	445229	BE278013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrogen	3.22
45	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
	414820	AA371831	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
	450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
	433233	AB040827	Hs.301804	Hs.301804:KIAA1494 protein	3.22
50	414172	AW954324	Hs.75790	(locuslink)NM_002842:Homo sapiens phosph	3.21
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
	447140	AF070537	Hs.17491	NM_138391:Homo sapiens hypothetical prot	3.21
55	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
	400836				3.20
	420281	AI623693	Hs.323494	(locuslink)NM_017984:Homo sapiens hypoth	3.20
	414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20
	447086	BE539188	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
60	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
	425281	BE385089	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:28333	3.20
	407736	NA1744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30577 fis	3.20
	400845				3.20
	407082	Z47055			3.20
65	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinase	3.20
	403217				3.20
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
	417777	AI829763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
70	457274	AW574193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.19
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	3.19
	430280	AA351258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
	422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protel	3.18
75	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
	449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
	425925	NM_001196	Hs.172894	Hs.172894:BH3 interacting domain death a	3.18
	414814	D14897	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
	405387				3.18
80	444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2)	3.17
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
	410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

5	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	3.17
	415032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nucleases (multifunctional	3.17
	417018	M16038	Hs.80887	Hs.80887:v-jes-1 Yamaguchi sarcoma viral	3.16
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regl	3.16
10	442843	U82758	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	3.16
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429566	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2665	3.16
	418127	BE243982	Hs.83532	(locuslink)NM_002388:Homo sapiens membra	3.15
15	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens Integr	3.15
	414702	L22005	Hs.76932	NM_004369:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flevohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
20	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
	407961	AW872939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-1	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolp	3.14
	450295	A1766732	Hs.210628	Hs.210628:ESTs	3.14
25	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780189	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451818	Hs.290216	Hs.290216:ESTs	3.13
30	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (transf a	3.13
	447627	AF090922	Hs.152738	NM_016950:Homo sapiens mitochondrial rib	3.13
	422753	A1928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H117182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	RA7479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
35	438444	A1064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3458	3.12
	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fs	3.12
	436975	AL118990	Hs.373654	(locuslink)NM_130786:Homo sapiens alpha-	3.12
	426690	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
	412326	R07588	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
40	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	3.12
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	3.12
	422675	BE018617	Hs.119140	NM_001870:Homo sapiens eukaryotic transl	3.12
	444301	AK000138	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	408932	A376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
45	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptobrevin 2	3.12
	413073	AL038166	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	405865	A1025931	Hs.181357	Hs.181357:latrunc receptor 1 (67kD, ribo	3.11
	405203				3.11
50	441028	A1333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	429824	AA296389	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168169	Hs.168169:bifunctional apoptosis regulat	3.11
55	408805	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	418976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003916	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
60	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	A1278802	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_008518:Homo sapiens solute carrier fa	3.10
	436472	AW972390	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
65	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	A1878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	3.10
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.10
70	427337	Z46223	Hs.176863	NM_005689:Homo sapiens Fc fragment of Ig	3.10
	433435	BE545272	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
	408150	BE520274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-4	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
75	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	3.09
	449051	AW981400	Hs.333626	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183683	NM_030666:Homo sapiens serine (or cyste	3.09
	430066	A1929659	Hs.237825	Hs.237825:signal recognition particle 72	3.09
80	428044	AA093322	Hs.301404	NM_005743:Homo sapiens RNA binding motif	3.09
	426989	A1815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine {	3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C27 protein	3.08

	410668	BE378794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisph	3.08
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
10	411423	AW845987	Hs.68864	(locuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin and/or	3.07
15	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG11	3.07
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	3.07
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	H69354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407167	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.06
	458814	AI488957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
20	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418052	AW630658	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (3.06
	407223	H98850		H98850:ycw03b12.s1 Soares melanocyte 2NbH	3.06
	418841	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
25	450690	AA296698	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYD d	3.06
	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
	436550	AI224458	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154872	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412867	AU076881	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA476986	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.46328	Hs.46328:fucosyltransferase 2 (secretor	3.05
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
	430508	AI015435	Hs.104837	Hs.104637:solute carrier family 1 (gluta	3.04
40	432261	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AW838306	Hs.128819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
	451711	AK000461	Hs.25890	NM_017829:Homo sapiens cat eye syndrome	3.04
45	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
	453460	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
50	412708	R26830	Hs.108137	Hs.106137:Homo sapiens mRNA for OK/SW-CL	3.04
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
	412527	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	444309	U83236	Hs.10803	Hs.10803:calcium and Integrin binding 1	3.03
55	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430954	AA954810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450807	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72864	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003728	Hs.19126	NM_003728:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 284	3.02
	417886	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355128	(locuslink)NM_144686:Homo sapiens hypoth	3.01
	424867	AI024880	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
70	437651	BE550672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	3.01
	438540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
	438000	AI825680	Hs.5595	Hs.5595:non-kinase Cdc42 effector protei	3.00
	415897	AI365603	Hs.279896	Hs.279896:DKFZP566H1024 protein	3.00
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
75	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406888	AA050445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
80	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rb-related anti	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
10	406685	Q_0	M18728
	432407	MH1429_12	BG036675 BF772005 BF771666 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157995 BE714315 AW818104 AW847619 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902156 AT732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986165 AK057283 BI881486 AA663341 AA457581 BG949294 AN392886 AA071122 AA227849 AA584918 BG959570 BF773486 ALD41698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF789107 BF804964 AW818172 AW818143 AW392930 AWB17057 AW858044 BF746211 AA178928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055692
15	459306	223120_4	AW578452
	452098	161393_1	BG028348 BF772844 HB3055 AW817969 H80985 BF755039 A185B183
	451129	1495511_1	BE072881 A1762181 BE072946

TABLE 11C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al" refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
30	406399	9256288	Minus	63448-63564
	403220	7630969	Plus	64338-64517
	403218	7630969	Plus	58039-58149
	403221	7630969	Plus	66294-66438,66936-67124
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	400529	9796988	Plus	138232-138423
35	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630969	Plus	61858-61995
	404626	6572184	Plus	47728-48046
	400750	8119067	Plus	198991-199168,199316-199548
40	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
45	404240	5002624	Minus	116132-116407,116653-116922
	402829	8918414	Plus	101532-101852,102006-102263
	406363	9256114	Plus	14403-14802,17000-17147,17241-17368
	402104	8119072	Plus	122409-122600
	402260	3398665	Minus	113785-113910,115653-115765,116808-11694
50	403912	7710730	Minus	72000-72280,72431-72700,72929-73199
	400836	8954179	Plus	677-1188
	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6687915	Minus	3769-3833,6708-6895
55	405203	7230116	Plus	125295-125463

60 Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59880 probesets on the Affymetrix/Eos-Hu03
 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the
 99th percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 99th percentile value amongst non-malignant tissues. In order to remove gene-
 specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before
 the ratio was evaluated.

TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

65	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
70	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
75	402075	U18557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
	435094	A1560129	Hs.329062	EST	30.3
	438606	W79123	Hs.68561	G protein-coupled receptor 87	28.8
80	452240	A1581147	Hs.61232	ESTs	27.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin bl	26.0
	417034	NM_006183	Hs.80962	neurotensin	25.5
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422958	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

	435505	AF200492	Hs.211238	interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (P13; serpin	20.1
5	452461	N78223	Hs.108105	transcription factor	19.8
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AJ678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW202886	Hs.261373	hypothetical protein dJ434014.3	16.3
10	428664	AK001688	Hs.189095	similar to SALL1 (sal (Drosophila))-like	16.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA806229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homo	15.4
	441459	AJ919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
15	447164	AF026941	Hs.17518	Homo sapiens cigs mRNA, partial sequence	13.8
	412749	AW016610	Hs.125911	ESTs	13.4
	417366	BE185288	Hs.1076	small proline-rich protein 1B (comifin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AJ023799	Hs.163242	ESTs	13.1
20	404956			Target Exon	13.1
	443211	AJ128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428518	AA885360	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
25	421478	AJ683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31162	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415969	AJ267700	Hs.317584	ESTs	11.5
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.226320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
	439926	AW014875	Hs.137007	ESTs	10.2
40	428388	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fls, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442860	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055611	Hs.226588	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057: Homo sapiens ZW10 Interactor (ZW10	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AA420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458184	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455501	AJ368680	Hs.816	SRV (sex determining region Y)-box 2	9.4
	418882	NM_004998	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	8.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
55	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fls, clone NT2RP40	9.1
	420502	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.0
	428427	M86899	Hs.169840	TTK protein kinase	9.0
	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
60	446232	AJ281848	Hs.194681	retinoic acid induced 3	8.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383082	Hs.1608	replication protein A3 (14kD)	8.9
65	430486	BE052109	Hs.241561	chloride channel, calcium activated, family m	8.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963		gbc:MR0-ST0032-200898-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
70	458027	L45054	Hs.85195	myeloid leukemia factor 1	8.4
	424066	AJ351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AJ624049		gbc:41a09.x1 NCLCGAP_Ut1 Homo sapiens cDNA	8.3
	406522	AJ541214	Hs.46320	Small proline-rich protein SPRK (human, odont	8.2
75	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423848	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
80	410044	BE586742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
	423228	AJ553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA668879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
	406654			Target Exon	7.4
5	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86817	ESTs	7.2
	446364	AB008824	Hs.14912	KIAA0286 protein	7.2
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
10	414148	BE084049		gb:PMO-BT0651-270400-003-f02 BT0651 Homo sapi	7.0
	429548	AW138872	Hs.135288	ESTs	7.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24598	RAD51-Interacting protein	7.0
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
15	431841	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.195729	ESTs	6.9
	450028	AIB12012	Hs.200737	ESTs	6.8
20	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
	413573	AJ733859	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
	454988	AW850140		gb:IL3-CT0219-281099-023-D11 CT0219 Homo sapi	6.8
25	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	409041	AB033025	Hs.50081	KIAA1199 protein	6.7
	407839	AA045144	Hs.161586	ESTs	6.6
	415852	T79213	Hs.272073	ESTs	6.6
30	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
35	431622	AW979271	Hs.293184	ESTs	6.5
	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	6.4
	414812	X72755	Hs.77367	monokine induced by gamma Interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
40	448435	AW205737	Hs.253562	ESTs	6.3
	421948	L42583	Hs.334309	keratin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	A1925153	Hs.217493	annexin A2	6.2
45	453884	AA359525	Hs.36232	KIAA0186 gene product	6.2
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142653	ret finger protein	6.1
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HEMBB10	6.1
50	427043	AA397679	Hs.3991	ESTs	6.1
	409723	AW885757	Hs.257862	ESTs	6.1
	459462	AA481396	Hs.105167	ESTs	6.1
	423244	AL038379	Hs.208602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
	427217	AA399272	Hs.144341	ESTs	6.0
55	441820	AA869119	Hs.143502	ESTs, Weakly similar to envelope protein [H.s	6.0
	437858	BE138550	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA488293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [H.s	5.9
	413395	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.9
60	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
	414299	AA142989	Hs.71730	ESTs	6.8
	439282	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin (140	5.8
	413825	AW451103	Hs.71371	ESTs	5.8
65	416048	AJ970536	Hs.16603	hypothetical protein FLJ13163	5.8
	415064	AA158804	Hs.149305	hypothetical protein MGC2803	5.7
	426895	NM_006401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	416900	Z43758	Hs.26037	ESTs	5.7
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
70	449611	AJ970394	Hs.197075	ESTs	5.7
	426637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
	438899	AJ278360	Hs.31409	ESTs	5.7
	414972	BE283782	Hs.77695	KIAA0008 gene product	5.7
75	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone COL0042	5.6
	407748	AK001862	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW253207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41680	desmocollin 3	5.5
	410959	AJ080175	Hs.68826	ESTs	5.5
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo sapi	5.5

	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
5	418502	R99288	Hs.35152	ESTs	5.4
	440320	AA879294		gb:mn86e09.s1 NC1_CGAP_Pr12 Homo sapiens cDNA	5.4
	439679	AF086400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gale	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
10	408768	NM_003686	Hs.47504	exonuclease 1	5.4
	451411	AA017492	Hs.135655	EST	5.4
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40489	dieckkopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB8 interacting, kinesin-like (rabkinesin 6)	5.2
15	420028	AI831190	Hs.166676	ESTs	5.2
	427356	AW023482	Hs.97849	ESTs	5.2
	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
20	445259	AI798994	Hs.152923	ESTs	5.2
	457345	AI699933	Hs.192175	ESTs	5.2
	453161	AA628608	Hs.61656	ESTs	5.2
	445019	AI205540	Hs.281285	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
	439706	AW872527	Hs.58781	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
25	431484	AA891355	Hs.296312	hypothetical protein DKFZp434A1315	5.2
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	5.2
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholera, al	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
30	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-inserte	5.1
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547			NM_018833*:Homo sapiens transporter 2, ATP-bl	5.1
	435206	AM32364	Hs.160594	ESTs	5.1
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
35	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
	413251	AI932903	Hs.211535	ESTs	5.1
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.1
	458629	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3'	5.0
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
40	432473	AI202703	Hs.152414	ESTs	5.0
	418736	AW388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016836	Hs.233364	ESTs	5.0
45	449448	D60730	Hs.67471	ESTs	5.0
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp588P2321 (from c	4.9
	405657			C7000246:gl 72477 pr DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI337228	Hs.197083	ESTs	4.9
50	434376	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetical	4.9
	421455	H87879	Hs.102267	lysyl oxidase	4.9
	443935	T88897	Hs.16845	ESTs	4.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
55	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-induc	4.8
	423673	BE003064	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
	441720	AI346487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
60	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
	428846	AB023021	Hs.225845	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
	418939	AW630903	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
65	433858	N68243	Hs.192874	hypothetical protein FLJ12735	4.7
	450434	AA166960	Hs.195870	hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516	fidgin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	4.7
70	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
	457465	AW301344	Hs.122908	DNA replication factor	4.6
	433159	AB036898	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937495		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapl	4.6
	401137			Target Exon	4.6
75	401575			Target Exon	4.6
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
80	450510	AA010056	Hs.242988	ESTs	4.6
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino acid	4.5
	449416	AI851016	Hs.246311	ESTs	4.5

5	416168	H23687	gb:yn72d12.1 Soares adult brain N2b5HB55Y Ho	4.5
	447033	AI357412	ESTs	4.5
	448353	AI250919	ESTs	4.5
	443715	AI583187	cyclin E1	4.5
	454707	AW814969	gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapi	4.5
10	435435	T89473	ESTs	4.5
	412099	U64198	interleukin 12 receptor, beta 2	4.4
	409731	AA125985	thymosin, beta, identified in neuroblastoma c	4.4
	422809	AK001379	hypothetical protein FLJ10549	4.4
	430919	AA489041	ESTs	4.4
15	435313	AI769400	ESTs	4.4
	425071	NM_013989	delodinate, iodothyronine, type II	4.4
	433322	H50621	ESTs, Weakly similar to I38022 hypothetical p	4.4
	416111	AA032813	chromatin assembly factor 1, subunit A (p150)	4.4
	408908	BE296227	serine/threonine kinase 15	4.4
20	444781	NM_014400	GPI-anchored metastasis-associated protein ho	4.4
	429170	NM_001394	dual specificity phosphatase 4	4.4
	414035	Y00630	serine (or cysteine) proteinase inhibitor, cl	4.4
	418216	AA682240	AF15q14 protein	4.4
	446252	AI283125	ESTs	4.4
25	447519	U46258	ESTs	4.4
	425916	NM_006786	urotensin 2	4.3
	409420	Z15008	laminin, gamma 2 (nicotin (100kD), kalinin (10	4.3
	416320	H47867	ESTs	4.3
	431808	M30703	amphiregulin (schwannoma-derived growth facto	4.3
30	441582	BE650200	ESTs	4.3
	414132	AI801235	ESTs	4.3
	424012	AW368377	tumor protein 63 kDa with strong homology to	4.3
	411835	U29343	hyaluronan-mediated motility receptor (RHAMM)	4.3
	433330	AW207084	hypothetical protein MGC14801	4.3
35	428813	AB037749	KIAA1328 protein	4.3
	425921	NM_007231	soluble carrier family 6 (neurotransmitter tra	4.3
	447078	AW885727	ESTs	4.3
	434699	AA643687	Homo sapiens cDNA FLJ11980 fis, clone HEMB310	4.3
	428758	AA433988	hypothetical protein FLJ14303	4.3
40	405708		Target Exon	4.3
	433405	AW157566	ESTs	4.3
	458443	AW987500	ESTs	4.3
	428479	Y00272	cell division cycle 2, G1 to S and G2 to M	4.2
	448821	AI097144	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
45	412808	AA247896	Homo sapiens clone TCCTA00151 mRNA sequence	4.2
	406587	M31126	pregnancy specific beta-1-glycoprotein 9	4.2
	455365	AW948343	gb:RCO-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
	452930	AW195285	ESTs, Weakly similar to I38022 hypothetical p	4.2
	430134	BE380149	ESTs, Weakly similar to T33188 hypothetical p	4.2
50	423035	AW449679	H.sapiens XG mRNA (clone PEP11)	4.2
	427686	AI791495	calmodulin-like skin protein	4.2
	444602	AI174455	ESTs, Moderately similar to I38022 hypothetic	4.2
	417791	AW965339	ESTs	4.2
	444286	AI424984	ESTs	4.2
55	438394	AA149250	ESTs	4.2
	457336	AW969657	ESTs	4.2
	429125	AA448854	ESTs, Weakly similar to I38022 hypothetical p	4.2
	404440		NM_021048:Homo sapiens melanoma antigen, fami	4.2
	449228	AJ403107	protein related with psoriasis	4.2
60	437144	ALD49468	ESTs	4.2
	448599	AW860912	gb:CVD-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
	431810	X67155	kinasin-like 5 (mitotic kinasin-like protein	4.2
	419991	AJ000098	eyes absent (Drosophila) homolog 1	4.2
	444361	W76027	hypothetical protein FLJ11105	4.2
65	458118	AW977549	KIAA1785 protein	4.1
	444105	AW189087	ESTs	4.1
	426010	AA136563	hypothetical protein FLJ21007	4.1
	409632	W74001	serine (or cysteine) proteinase inhibitor, cl	4.1
	408086	BE250182	dihydrofolate reductase	4.1
70	457520	AA602711	EST	4.1
	402048		Target Exon	4.1
	427025	AA397589	ESTs	4.1
	423515	AA327017	ESTs	4.1
	423891	AK002042	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
75	455310	AW893981	gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
	418696	AW939433	hypothetical protein FLJ12581	4.1
	426642	AW058223	ubiquitin C-terminal hydrolase UCH37	4.1
	423738	AB002134	airway trypsin-like protease	4.1
	448243	AW369771	integrin, beta 8	4.1
80	411559	BE144081	gb:MR0-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
	423553	AA405635	ESTs, Weakly similar to DYX_HUMAN CYTOPLASMI	4.1
	457030	AI301740	dihydropyrimidinase-like 2	4.1
	424115	AA335497	ESTs, Weakly similar to I38022 hypothetical p	4.1
	432374	W68815	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
	424745	AA214618	activator of S phase kinase	4.0
	433384	AK021892	ESTs	4.0
	448995	AI613276	guanine nucleotide binding protein (G protein	4.0

	448504	A1858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
	424794	M85646	Hs.210696	ESTs	4.0
5	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	cortistatin	4.0
	417891	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	A1553695	Hs.159422	Homo sapiens cDNA FLJ13987 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
15	415857	AA868115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	AI422017		gb:45f12.x1 NCL CGAP_Bm23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0517	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283361	ESTs	3.9
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177877	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959			NM_025001*:Homo sapiens hypothetical protein	3.9
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 (H.sapi	3.9
	432757	AF113013	Hs.278919	PRO0806 protein	3.9
30	418686	Z36830	Hs.87268	annexin A8	3.9
	437845	AA769578	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.8
	415312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204086	lipophilin B (uteroglobin family member), pro	3.9
35	410563	AW016824	Hs.255527	hypothetical protein MGC14128	3.8
	444665	BE13126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AJ791749	Hs.128596	ESTs	3.9
	438656	H85310	Hs.209458	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
40	406560			ENSP00000016943*:CDNA	3.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	408601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46658	ESTs	3.8
45	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
	436149	AI754308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-blind	3.8
	405545			(MDRVAP) (TAP2)	3.8
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409687	T51125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001821	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidamylasts bu	3.7
	405943			Target Exon	3.7
60	430588	NM_001942	Hs.2633	desmoglein 1	3.7
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465884	Hs.280728	ESTs	3.7
	449592	A1655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
	418735	N48789	Hs.44809	ESTs	3.7
70	444707	AI188813	Hs.41680	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055		gb:tg20g10.x1 NCL CGAP_U11 Homo sapiens cDNA	3.7
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
75	432837	AA310893	Hs.87329	HSPC072 protein	3.7
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	A1806335	Hs.200829	ESTs, Weakly similar to T30171 ninetin - mouse	3.7
80	410784	AW803201		gb:IL2-UM0077-0705G0-080-E08 UM0077 Homo sapi	3.7
	409582	R27430	Hs.271585	ESTs	3.6
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

5	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BTU631-180200-078-c08 BT0531 Homo sapi	3.6
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
10	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE35 gene	3.6
	413278	BE583085	Hs.833	Interferon-stimulated protein, 15 kDa	3.6
	420373	AW588228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
15	424296	AI031874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
	434321	AA629368		gb:zu78a11.s1 Soares_Jasits_NHT Homo sapiens	3.6
	426514	BE016833	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
20	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/24kD)	3.6
	426749	AI623718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin I	3.6
25	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin (H.sapi	3.6
	424927	AW873886	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin t	3.5
	408867	AA437199	Hs.656	cell division cycle 25C	3.5
	428508	BE252363	Hs.184668	SBB131 protein	3.5
30	431120	AA492568		gb:ng93c08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557*:Homo sapiens keratin 16 (focal non	3.5
	409695	AA288961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTPMP10 (HT	3.5
35	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.118991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
	443113	AI040686	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8688	ESTs	3.5
40	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
	408633	AW963372	Hs.46677	PRO2000 protein	3.5
	427878	C05766	Hs.181022	CGI-07 protein	3.5
45	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen tNFLS	3.5
	411274	NM_002776	Hs.69423	kalikrein 10	3.5
	400666			NM_002425:Homo sapiens matrix metalloproteinase	3.5
50	426820	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
55	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.336799	ESTs	3.4
	419807	R77402		gb:yl75f11.s1 Soares placenta Nb2HP Homo sapi	3.4
	451778	AB261131	Hs.71243	ESTs, Weakly similar to zinc finger protein [3.4
60	430387	AB24533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23950	cyclin B1	3.4
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.4
65	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045548	Hs.301957	nucleic (nucleoside diphosphate linked motif X	3.4
	434206	AW138973	Hs.288516	ESTs, Weakly similar to S68890 mitogen induc	3.4
	413219	AA876200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
70	422487	AJ010901	Hs.188267	nucln 4, tracheobronchial	3.4
	438993	AA828995		gb:cd77b08.s1 NCL_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
	435360	AF105386	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	426572	AB087783	Hs.170623	hypothetical protein FLJ11183	3.4
75	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AI054680	Hs.171176	ESTs	3.3
	444910	AI201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens cDNA	3.3
	426269	H15302	Hs.168950	Homo sapiens mRNA: cDNA DKFZp586A1046 (from c	3.3
	448101	AA205847	Hs.23016	G protein-coupled receptor	3.3
80	418994	AA286520	Hs.89548	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE068	3.3
	419751	AW195581	Hs.93121	KIAA0761 protein	3.3
	404782			C7001892*gl 6724096 gb AAAF26844.1 (AF195021	3.3
	415813	R20233		gb:yg18h11.r1 Soares infant brain tNIB Homo s	3.3
	452188	AI097660	Hs.61210	ESTs, Weakly similar to t38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

5	412879	BE082219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55608	ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895	ESTs	3.3
	443903	AI220547	Hs.135223	ESTs	3.3
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (from c	3.3
10	447153	AAB05202	Hs.315562	ESTs	3.3
	450769	AA057418	Hs.33654	ESTs	3.3
	421379	Y15221	Hs.103982	small Inducible cytokine subfamily B (Cys-X-C	3.3
	402481			NM_001821*:Homo sapiens choroideremia-like (R	3.3
	459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
15	424384	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495	ESTs	3.3
	414869	AA157291	Hs.21479	ubiquitin 1	3.3
	441690	RB1733	Hs.33106	ESTs	3.3
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
20	412246	AI160873	Hs.69233	zinc finger protein	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
	451177	AI989716	Hs.13034	ESTs	3.3
	409990	AA079337		gb:zm95b09.r1 Stratagene colon HT29 (937221)	3.3
25	418462	BE001696	Hs.85266	Integrin, beta 4	3.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196			C2000682*:g[7512792]pir[12482] hypothetical	3.3
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
	432917	NM_014125	Hs.279812	PRC0327 protein	3.3
30	448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307	ESTs	3.3
	420218	AW958037	Hs.286	ribosomal protein L4	3.2
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fls, clone HEMBB10	3.2
	447762	AI939461	Hs.161370	ESTs	3.2
35	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323345	KIAA1008 protein	3.2
	402800			Target Exon	3.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
40	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
	401458			Target Exon	3.2
	432381	AI378582	Hs.159585	ESTs	3.2
45	444008	BE544865	Hs.220758	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
	405336			Target Exon	3.2
	446563	BE326588	Hs.141464	ESTs	3.2
	449278	AW241510	Hs.252713	ESTs	3.2
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
50	420591	X53655	Hs.99171	neurotrophin 3	3.2
	401488			C4000647*:g[4758508]ref[NP_004253.1] airway	3.2
	432979	AA573263	Hs.120860	ESTs	3.2
	413633	Z15005	Hs.75573	centromere protein E (312kD)	3.2
	438325	AA804258	Hs.123229	ESTs	3.2
55	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
	431938	AA838471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
	421777	BE562088	Hs.108195	HSPC037 protein	3.2
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fls, clone ADKA02	3.2
	427359	AW020792	Hs.79981	Homo sapiens cDNA: FLJ23008 fls, clone LNG004	3.2
60	402337			Target Exon	3.2
	420930	AW888650		gb:CMA-NT0007-130600-551-406 NT0007 Homo sapi	3.2
	438168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fls, clone HEMBA10	3.2
	443428	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
	437641	AA811452	Hs.201911	ESTs	3.1
65	414761	AJ077228	Hs.77255	enhancer of zeste (Drosophila) homolog 2	3.1
	434208	T92641	Hs.127648	hypothetical protein PRC2176	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
	458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
70	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
	439750	AL355053	Hs.57664	Homo sapiens mRNA full length insert cDNA clo	3.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
	445886	AI734008	Hs.127699	KIAA1803 protein	3.1
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fls, clone HEP010	3.1
75	424653	AW977534	Hs.151459	calcium/calmodulin-dependent serine protein k	3.1
	431322	AW970522		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	423934	U89965	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
	455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
80	423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
	408295	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084	ESTs	3.1
	441974	AI683782	Hs.128245	ESTs	3.1
	446474	AJ301227	Hs.150186	hypothetical protein DKFZp565K1946	3.1
	452166	AI948607	Hs.264880	ESTs	3.1
	451659	BE379761	Hs.14248	ESTs	3.1
	439979	AW500291	Hs.6823	hypothetical protein FLJ10430	3.1

	447701	BE619525	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AJ085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
5	449441	AI656040	Hs.195532	ESTs	3.1
	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
10	440953	AI683038	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NY2RP30	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	HA6739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	mlnchromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
15	419563	AA528235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp596L1121 (from c	3.1
	435604	AA625279	Hs.28892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178086	Hs.144081	ESTs	3.1
	435081	AI651474	Hs.163944	ESTs	3.1
20	420589	AA419380	Hs.192708	ESTs	3.0
	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
	406087			Target Exon	3.0
25	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnanLularus_NbHPU Ho	3.0
	435590	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163800	ESTs	3.0
30	448733	NM_005829	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950067		gb:wg05c02.x1 NCL CGAP_K6d12 Homo sapiens cDN	3.0
35	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
	434808	AF155108	Hs.256160	Homo sapiens, similar to RIKEN cDNA 2810027O1	3.0
	445505	AI971156	Hs.148891	ESTs	3.0
	426005	AI565851		gb:tn07g03.x1 NCL CGAP_Bm25 Homo sapiens cDN	3.0
	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
40	432189	AA527941		gb:nh30c04.s1 NCL CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AI040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE076114		gb:FM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
45	417734	Z42667	Hs.6724	ESTs	3.0
	449676	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:UH-H-BH2-ehv-h-03-0-ULs1 NCL CGAP_Sub4 Ho	3.0
50	444477	AI150548	Hs.23155	ESTs	3.0
	448255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gil75131 t3 pir T13078 KIAA0892 pro	3.0
	450841	AJ741468	Hs.270515	ESTs	3.0
	410581	BE540265	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
55	433871	W02410	Hs.205555	ESTs	3.0
	401994			Target Exon	3.0
	448272	AW137656	Hs.197845	ESTs	3.0
	409703	NM_008187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (160 kD)	3.0
	400250			Eos Control	3.0
60	408915	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	BE284833	Hs.143638	WD repeat domain 4	3.0
	432220	AJ571306	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:bb75d03.x1 NCL CGAP_U12 Homo sapiens cDNA	3.0
65	447313	U92981	Hs.18081	Homo sapiens clone DTIP186 mRNA, CAG repeat	3.0
	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; tr	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
70	433485	AJ493078	Hs.201967	aldo-keto reductase family 1, member C2 (dihy	3.0
	423566	R72894	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	3.0
	426880	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
75	402558			C1001383:gil538695 pir A51183 hypothetical	2.9
	411098	AW817238		gb:QV0-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	435399	AA679463		gb:ac50c03.x1 Stralagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	NA5214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
	410658	AW105231	Hs.192035	ESTs	2.9
80	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621*Keratin, type II cytoskeletal	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

	455319	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407658	AJ404672	Hs.334483	hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654	ESTs	2.9
5	432215	AJ076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.9
	434423	NM_006769	Hs.3844	LIM domain only 4	2.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.9
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583	Homo sapiens cDNA FLJ20779 fs, clone COL0507	2.9
10	421190	U95031	Hs.102482	mucln 5, subtype B, tracheobronchial	2.9
	404981			ENSP0000025242*:Keratin, type II cytoskeletal	2.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced by lu	2.9
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760			Target Exon	2.9
15	443859	NM_013409	Hs.9914	folliculin	2.9
	404253			NM_021058*:Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	2.9
	436887	AA954229	Hs.114052	ESTs	2.9
	429036	BE549781	Hs.270475	ESTs	2.9
20	446733	AA653360	Hs.26040	ESTs, Weakly similar to fatty acid omega-hydr	2.9
	446417	AJ299050		gb:xn14d12.x1 NCL CGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.9
	452452	BE393822	Hs.29645	Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178	hypothetical protein FLJ23488	2.9
25	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypothetical p	2.9
	439430	AF124250	Hs.6564	cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502	ESTs	2.9
	401781			Target Exon	2.9
30	439825	AF086453	Hs.68611	ESTs	2.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153	ESTs	2.9
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AI688594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
35	443479	AF027219	Hs.8443	zinc finger protein 202	2.9
	442601	AI684969	Hs.46772	ESTs	2.9
	405932			C15000305:q[3806122]b[AAC69198.1] (AF097887	2.9
	405454			C12000541:g[5729884]ref[NP_006539.1] IGF-II	2.9
40	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	2.9
	408552	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.45384	heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010	ESTs	2.9
	411268	AK000512	Hs.69388	hypothetical protein FLJ20505	2.9
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_1NFLS	2.9
45	400297	AH127076	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	2.9
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.9
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.263713	ESTs, Weakly similar to S64054 hypothetical p	2.9
50	436711	AF226657	Hs.65553	CTP synthase II	2.9
	419088	AIS38323	Hs.52620	Integrin, beta 8	2.8
	431629	AJ077025	Hs.265927	Interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984	hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503	ESTs	2.8
55	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.8
	405281			NM_002864:Homo sapiens pregnancy-zone protein	2.8
	438161	BE089028	Hs.20158	ESTs, Weakly similar to S34169 transcription	2.8
	409103	AF251237	Hs.112208	XAGE-1 protein	2.8
	425599	AW336745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
60	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mif5, S	2.8
	435099	AC004770	Hs.4765	flap structure-specific endonuclease 1	2.8
	445873	AA250870	Hs.251946	poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216	ESTs	2.8
	413083	BE064528		gb:RC4-BT0311-250200-014-h08 BT0311 Homo sapi	2.8
65	437030	AA742577	Hs.303781	EST	2.8
	438113	AI467908	Hs.8882	ESTs	2.8
	442873	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23158 fs, clone LNG096	2.8
	440994	AI180011	Hs.193341	ESTs	2.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fs, clone HEMBA10	2.8
70	422689	AW856665		gb:RCS-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin, tissu	2.8
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.161275	ESTs	2.8
	403806			Target Exon	2.8
75	437182	AL080098		gb:Homo sapiens mRNA; cDNA DKFZp584C1072 (fro	2.8
	453955	AW579207	Hs.304666	ESTs, Weakly similar to I78885 serine/threonin	2.8
	420795	AA323037	Hs.128645	sorting nexin 16	2.8
	452696	AI826645	Hs.211534	ESTs	2.8
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.8
80	438052	AA776564	Hs.41891	zinc finger 1111	2.8
	441755	AW450826	Hs.127786	ESTs	2.8
	427981	AW293165	Hs.143134	ESTs	2.8
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072	ESTs	2.8

	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.8586	thyroid hormone receptor interactor 13	2.8
5	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
	448979	AI611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250718	Hs.87614	ESTs	2.8
10	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	AI267371	Hs.172636	ESTs	2.8
	469719	AW749611	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144587	Homo sapiens cDNA FLJ12981 fs, clone NT2RP20	2.8
15	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
20	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026435	Hs.177534	dual specificity phosphatase 10	2.8
	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34685	ESTs	2.8
25	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
	426343	NM_014642	Hs.189387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418692	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
30	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fs, clone MAMMA10	2.7
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetical	2.7
35	406753	AA505865	Hs.217493	annexin A2	2.7
	415747	AA381209		gb:EST94257 Activated T-cells 1 Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430486	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
40	456181	L36463	Hs.1030	ras inhibitor	2.7
	416548	H62953		gb:u47708.r1 Scores fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
45	417398	N78541	Hs.177366	ESTs	2.7
	408380	AF123050	Hs.44532	diubiquitin	2.7
	437724	AW444828	Hs.184323	ESTs	2.7
	406680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7
50	441362	BE514410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli RecA ho	2.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
	408092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
55	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
	446839	BE081926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	406675			Target Exon	2.7
	424825	AW004466	Hs.321197	PDZ domain protein (Drosophila InaD-like)	2.7
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
60	448592	N69546	Hs.44563	hypothetical protein	2.7
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fs, clone MAMMA10	2.7
	407287	AI678812		gb:u59408.x1 NCLCGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	412977	AA125910	Hs.181461	ESTs	2.7
65	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
	417357	AF280257	Hs.131917	retinitis pigmentosa GTPase regulator Interac	2.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	D66980	Hs.79170	KIAA0227 protein	2.7
	458201	AI989981	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
70	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
	401230			NM_014191*Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	462747	BE153855	Hs.61460	lg superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234642	aquaporin 3	2.7
75	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
	443500	AV646388	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neurexin B	2.7
	445640	AW989628	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
	418889	AW516655		gb:xq01d05.x1 Scores_NHCCc_cervical_tumor Hom	2.7
80	431688	AA513906		gb:xq07c08.s1 NCLCGAP_Lp2 Homo sapiens cDNA	2.7
	427579	AA366143	Hs.179689	hypothetical protein FLJ20637	2.7
	423175	W27585	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI603886	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AI335361	Hs.228376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
5	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
	446102	AW168067	Hs.252958	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27498	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	2.6
	428082	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276886	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
15	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW884542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [Hs	2.6
20	401260			C1001031*.gq7305041 ref NP_038876.1 erythro	2.6
	435136	R27299	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW206878	Hs.29543	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA888176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e08.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
	405671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
30	460983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF148074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
35	408625	AW243323	Hs.266785	ESTs	2.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (360/400kD, mitotin)	2.6
40	401050			NM_014156*.Homo sapiens HSPC053 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE092900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_JHUMAN ZINC FINGER	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903*.Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	425698	NM_018112	Hs.159241	polycystic kidney disease 2-like 1	2.6
50	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93900	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U80304	Hs.25351	Iroquois homeobox protein 6	2.6
55	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
	408391	AW889276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427088	AB032953	Hs.173580	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
60	453391	AI240665	Hs.8895	ESTs	2.6
	447175	AI385208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288938	RAB22A, member RAS oncogene family	2.6
	418282	AA215536	Hs.98133	ESTs	2.6
65	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435853	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
70	418067	AI127858	Hs.83393	cystatin E/M	2.6
	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55644		gb:Human spleen PABL (pseudautosomal boundar	2.6
75	430994	AA490346	Hs.40530	Homo sapiens, clone MGC17624, mRNA, complete	2.6
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434C1214 (from c	2.6
	425415	M13903	Hs.157091	involucrin	2.6
80	444826	AI674482	Hs.148441	ESTs	2.6
	413331	BE083950		gb:PMO-BT0551-260200-001-b11 BT0551 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706*.gq1345652 sp P15989 CA3B_CHICK COL	2.6
	413864	BE175582		gb:RC5-HT0580-100500-022-CD1 HT0580 Homo sapi	2.6

	438746	AI885816	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.336951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1569	UIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.83002	ubiquitin carrier protein E2-C	2.5
	437412	BE059288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C138 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455548	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
15	409676	AA077118	Hs.197288	NS1-binding protein	2.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE814743	Hs.148688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.178312	small nuclear RNA activating complex, polypep	2.5
20	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
25	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
	407103	AA424861	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW298024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035281	Hs.61753	ESTs	2.5
30	438533	AI440286	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	448300	AI656959	Hs.222165	ESTs	2.5
35	434813	AW872860	Hs.11056	RALBP1 protein	2.5
	448946	AI662855	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
	449344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE150006	Hs.212296	ESTs	2.5
45	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.182843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	AI761324		gb:wl80b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_019371	Hs.71879	Interleukin 19	2.5
55	436861	AW376974	Hs.156704	ESTs	2.5
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
60	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300692	v-myb avian myeloblastosis viral oncogene hom	2.5
	442986	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	416327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA917808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE520811	Hs.126869	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435847	AI653240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
75	422565	BE258036	Hs.118400	slinged (Drosophila)-like (sea urchin fascic h	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88653	hypothetical protein FLJ10545	2.5
	408853	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AK053464	Hs.166505	ESTs	2.5
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
80	438214	H06076	Hs.26320	TRABID protein	2.5
	448745	AW118189	Hs.155400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

Key: Unique Eos probaset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407642	1007176_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806969 AW845688 BE141054 BE141040 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178969
408391	1055687_1	AW859276 AW859274 AW190959 T91463
408690	107490_1	AW864542 AA056567 AW882724
409594	114249_1	AA076118 AA975618 AA076220
409895	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409990	116644_1	AA079337 AA079338 AW272100
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW579476 AW939664 AW939665
410784	1221005_1	AW803201 BE079700 BE062940
411098	1232093_1	AW817238 AW993985 AW993998
411171	1234393_1	AW820260 AW820332 R94406
411465	1246768_1	AW847683 AW847861 AW861080
411559	1249417_1	BE144081 BE144190 AW851155
411819	1259748_1	AW947884 AW947918 AW947888 AW947893 AW947897 AW947910 AW947905 AW864751 AW947878
411858	126717_1	AA099020 AW751275 AW751276 AW751289
412279	1287332_1	BE245511 BE246133 AW935247
412313	1289355_1	AW936832 AW936809 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819 AW937485 AW937589 AW937658 AW937654 AW937492 AW945964 AW946020 AW946034 AW948027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039
412333	1289037_1	
412387	1291505_1	AW846045 AW946028 AW948038
412879	1334272_1	BE092219 BE092361 BE006789
413083	1348639_1	BE084528 BE084589 BE064561
413331	1361726_1	BE083950 BE084017 BE084016
413864	1395788_1	BE175582 BE175514 BE175505 BE175591 BE175530
414147	142127_1	BE091634
414148	142133_1	BE084049 AW292907 AA135984
416317	1533847_1	Z43388 F05453 R19373 R20275 H06917
416813	1540602_1	R20233 F12901 T74740
415747	155189_1	AA381209 AA381245 AA167683
416120	1571266_1	H46739 H51513 H19779
416168	1574545_1	H23587 H46460 H40239
416548	1600181_1	H62953 N76908 N72413
417742	1695282_1	R64719 Z44880 R12451
418347	174149_1	AA216419 F03238 AA229517
418869	179863_1	AW516585 AA229782 AA230035
419007	188252_1	R77402 AA262462 AA260988 R06794
420373	193194_1	AW968228 AA259146 W01465
420837	195241_1	AW976163 AA278945 AA747691
420890	197736_1	AW888850 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422689	219898_1	AW856656 AA315008 AW954733
423733	231476_1	AA330281 AA330232 AW962521
423735	231498_1	AA330269 AA661806 AA502431 AW974633 AA649496
423841	232507_1	AW753967 AA370785 AA331630 AW962550
425005	245908_1	AI565851 AA348656 R24798
429163	300543_1	AA884766 AW974271 AA592975 AA447312
431120	328264_1	AA492588 AA492498 AA492571
431322	331543_1	AW970622 AA503009 AA502998 AA502988 AA502805 T92188
431688	336809_1	AA513906 AA847734 AI357044
432184	342677_1	AW971125 AA527731 N62655 AI821608 AA532420
432189	342819_1	AA527941 AI810608 AI620190 AA635286
432869	355475_1	AW974094 AA569074 AA602574
433289	36202_1	AF006258
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433644	371919_1	AW342028 AA641080 AA603282
434321	383473_1	AA625368 AW849574 AW849573
435399	405576_1	AA679463 AW813779 AW813709
437182	43421_1	AL080098 AL037472 AA432051
437938	44673_2	AI950087 N70208 R97040 N38809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34726 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW236363 AA688345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA688777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI981530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75828 N22388 H84729 H60052 T82487 AI022050 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AM23279 AI423646 AI424090 AI359637 ALD44732 D17003 AW978074 AA834841 AA828650 AA828995 AA834879 AI926361
438390	45662_1	
438966	467436_1	
438993	467651_1	

439579 47404_1 AF086400 W79232 W73990
 440320 491930_1 AA879294 N67538 A474541
 444910 624951_1 AL201849 BE069007 AW946544
 446417 676384_1 AI299050 BE256910
 447197 711623_1 R36075 AI366546 R36167
 448699 770766_1 AW860912 AI540856
 449034 794817_1 AH24049 AW117770 AI858360
 450024 82298_1 AA005129 AA679084 AA694399
 450613 840016_1 AI702055 R89204 R86260
 451105 859083_1 AI761324 AW880941 AW880937
 451153 88054_1 BE092900 AA015877 AA018521
 451340 86640_1 AW936273 AW340350 AA017208
 454202 1050507_1 AW178363 AW846011 AW845964 AW845985 AW845977 AW846002
 454241 1067807_1 BE144668 BE184942 AW238414 BE184946
 454707 1230250_1 AW814988 AW814852 AW814808
 454891 1239217_1 AW837349 AW837355 AW882717
 454988 1248607_1 AW850140 AW850195 AW850192
 455091 1252939_1 BE079752 BE079868 BE149989 AW855532 BE148818 BE148815 BE148796
 455092 1252971_1 BE152428 AW855572 AW855607
 455095 1252987_1 AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855696 AW855610 AW855601 AW855605
 455203 1258973_1 AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865390 AW865390
 455310 1278158_1 AW893961 AW893998 AW894034 AW894019
 455319 1279172_1 AW895387 AW895647 AW895664 AW895323 AW895405 AW895639 AW895638
 455385 1284681_1 AW948343 AW948341 AW902855 AW984737
 455549 1324696_1 AW994222 AW994377
 456666 1349545_1 BE065813 BE065788 BE066889 BE065832
 456750 1356993_1 BE075114 BE075283 BE075118
 455838 1374605_1 BE145808 BE145807 BE181883
 456987 1397735_1 BE178323 BE177978
 457405 333127_1 AA504860 AA504911
 458829 773443_1 AI557388 BE158938
 459267 966605_1 AJ003631 AJ003650 AJ003651

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset.
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400612	9929646	Minus	151513-151662
400666	8118496	Plus	17982-18115,20297-20456
401050	8117828	Minus	78449-79425
401137	2547238	Minus	598-1009
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401260	8076883	Minus	88008-85355
401367	9786188	Minus	145358-145807
401458	9157896	Plus	76485-77597
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401576	7228804	Minus	76263-76384
401747	9789672	Minus	118598-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133560-134011
401760	9929699	Plus	63126-83250,85320-85540,94719-95297
401780	7249190	Minus	28397-28617,28920-29045,29135-29250,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86614
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402048	8072512	Plus	43936-44078
402298	6598824	Plus	36768-37953
402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
402481	9797406	Plus	87681-88991
402556	9863723	Plus	13579-14026
402638	9958129	Minus	20167-22383
402800	6010175	Plus	43921-44049,46161-46273
402892	8086844	Minus	194384-194645
403274	8072441	Minus	104069-104170,105683-106859
403471	9930659	Minus	85867-85983
403763	7229888	Minus	43675-43887
403808	8140491	Plus	146390-146678
403983	8576059	Minus	82441-82701
404107	8059028	Minus	201699-202363
404132	6981900	Plus	11307-12434
404184	4581418	Minus	12652-13548
404253	9367202	Minus	55675-56055
404440	7528051	Plus	80430-81581
404782	9910084	Minus	15455-15589
404959	7407964	Plus	45243-45368
404981	4432779	Minus	20826-20770,22613-22721
404986	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405041	7547195	Plus	121230-121714
405196	7230083	Minus	135716-135851

	405277	3980473	Plus	23471-23572
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-46958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405336	6094635	Plus	33267-33563
5	405454	7656675	Plus	133807-134053
	405545	1054740	Plus	118577-118907,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	405657	4827303	Minus	104132-104293
	405675	4557087	Plus	70304-70630
10	405708	4156182	Plus	55030-55604
	405897	6758795	Plus	59826-60535
	405932	7767812	Minus	123525-123713
	405943	6758796	Plus	20605-20812
	406087	9123919	Minus	7234-7626
	406092	9123919	Plus	251370-251797,252168-252862
15	406457	8785551	Plus	182212-182958
	406554	7711556	Plus	106956-107121
	406560	7711559	Minus	35162-35292
20	406599	8248616	Plus	10933-11086

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. Ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Key: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 PPDomains: Predicted Protein Domains
 Unigen Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Key	ExAccn	UnigenID	PPDomains	Unigen Title	R1
425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_tern	desmoglein 3 (pemphigus vulgaris antigen)	43.6
418007	M13509	Hs.83189	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
438506	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
452240	A1591147	Hs.61232	TM	ESTs	27.0
424046	AF027865	Hs.138202	SS,TM,serpin	serpin (or cysteine) proteinase inhibitor	24.5
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin	20.5
418345	AJ001898	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(P113; se	20.1
423017	AW178761	Hs.227948	SS,serpin	serpin (or cysteine) proteinase inhibitor	19.2
428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys	15.9
447164	AF026941	Hs.17518	TM,IIR	Homo sapiens c1g5 mRNA, partial sequence	13.8
414764	AW013887	Hs.72047	TM	ESTs	12.9
418661	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
427585	D31152	Hs.179729	SS,C1g,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
406467			TM,effhand	Target Exon	10.5
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
418882	NM_004896	Hs.89433	TM,ABC, membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
419247	S65791	Hs.89764	TM,IH4-domain	fragile X mental retardation 1	9.1
446232	A1281848	Hs.194881	TM,7tm_3,ribosomal_L13	retinoic acid induced 3	8.9
424905	NM_002497	Hs.153704	TM,pklnase	NIMA (never in mitosis gene a)-related ki	8.9
422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamily	8.7
427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
447342	AJ198268	Hs.19322	SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.6
407839	AA045144	Hs.181586	TM,cadherin,Cadherin_C_tern	ESTs	6.6
410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma interferon	6.4
421773	W69233	Hs.112457	SS	ESTs	6.2
413385	M34455	Hs.840	TM,IDO	indoleamine-pyrrole 2,3 dioxygenase	5.9
413763	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short	laminin, beta 3 (p120 (125kD), laminin	5.8
432239	X81334	Hs.2536	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
418663	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
407366	AF026942		TM,IIR	gb:Homo sapiens c1g33 mRNA, partial seque	5.5
433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Ca10n_ATPase_C, N	ESTs	5.4
420440	NM_002407	Hs.97644	SRORUteroglobin	mammaglobin 2	5.2
437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
405547			SS,TM,ABC, membrane,ABC_tran,Ig	NM_018833*:Homo sapiens transporter 2, AT	5.1
439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
423634	AW959808	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
428350	NM_003245	Hs.2022	TM,Transglutaminin_C,Transglutaminin_N,Transglu_core	transglutaminase 3 (E polypeptide, protel	5.0
409744	AW675258	Hs.56265	TM,metallo,Kelch	Homo sapiens mRNA: cDNA DKFZp586P2321 (fr	4.9

444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon-I	4.8
423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,homopexin	matrix metalloproteinase 12 (macrophage e	4.8
450375	AA009647	Hs.8860	TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domai	4.8
401575	NA		TM	Target Exon	4.6
428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
425071	NM_013889	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
434899	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
406687	M31126	Hs.272620	SS,Peptidase_M10,homopexin	pregnancy specific beta-1-glycoprotein 9	4.2
404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
444105	AW189087	Hs.166597	TM,cadherin	ESTs	4.1
409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
423738	AB002134	Hs.132185	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
423553	AA405635	Hs.96854	TM	ESTs, Weakly similar to DYLLX_HUMAN CYTOPL	4.1
445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
446989	AK001898	Hs.18740	TM	hypothetical protein FLJ11036	4.0
428536	AI143139	Hs.2288	TM,efhand,Syndecan	visinin-like 1	3.9
413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
429441	AJ224172	Hs.204096	Uteroglobulin	lipophilin B (uteroglobulin family member),	3.9
409601	AF237621	Hs.80828	TM,filamentation,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
439238	N47305	Hs.46668	TM	ESTs	3.8
446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
405645			SS,TM,proteasome,Ig,ABC_memb,tranABC_tran,	(MDR1AP) (TAP2)	3.8
422936	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
423217	NM_000094	Hs.1640	SS,TM,in3,vwa,Collagen,Kunitz_BPT1	collagen, type VII, alpha 1 (epidermolytic	3.7
430586	NM_001942	Hs.2633	SS,TM,cadherin,Cadherin_C_term	desmoglein 1	3.7
444707	AI188613	Hs.41690	TM,cadherin	desmocollin 3	3.7
409682	R27430	Hs.271565	TM	ESTs	3.6
408771	AW732573	Hs.47584	TM,K_tetra,Ion_trans	potassium voltage-gated channel, delayed-	3.6
400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
413278	BE563085	Hs.833	TM,ubiquitin,aminin_G,aminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
408591	AF015224	Hs.46452	SS,TM,Uteroglobulin	mammaglobin 1	3.5
407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
407137	T97307		TM,GDA1_CD39	glycyl53h05.s1 Soares fetal liver spleen 1	3.5
411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
400686			SS,homopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acyltransf	endothelial cell growth factor 1 (platelet	3.4
450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
451778	AI826131	Hs.71243	Ig	ESTs, Weakly similar to zinc finger prote	3.4
430397	AI824533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
422487	AJ010901	Hs.198267	TM,vwd	mucin 4, tracheobronchial	3.4
449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
418894	AA296520	Hs.89646	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin 3, type 1, P-cadherin (placental	3.3
418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	integrin, beta 4	3.3
424887	J05070	Hs.151738	SS,Peptidase_M10,fn2,homopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
401486	NA		SS,TM,trypsin	C4000647:gi4768508:ref(NP_004253.1) air	3.2
408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23008 fis, clone LN	3.2
452934	AA581322	Hs.4213	SS,TM,Ig	hypothetical protein MGC16207	3.1
448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectinrm	Homo sapiens mRNA full length insert cDNA	3.1
414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
435804	AA625279	Hs.28892	TM	uncharacterized bone marrow protein BM040	3.1
453883	AI638516	Hs.22630	TM,Ets,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
448733	NM_005629	Hs.187958	SS,TM,SNF_ABC_tran,iodh,pkinase,DSPC,Ribosomal	solute carrier family 6 (neurotransmitter	3.0
444948	AW139205	Hs.168457	SS,TM,alcoholase	hypothetical protein FLJ22408	3.0
437938	AI950087		TM,histone,Ig,MHC_I	gb:wg05c02.x1 NCI_CGAP_Jd12 Homo sapiens	3.0
424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
409703	NM_006187	Hs.58009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
447313	U82981	Hs.18081	TGF-beta	Homo sapiens clone DT1P186 mRNA, CAG repe	3.0
431070	AW408184	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
421190	U95031	Hs.102482	TM,vwd	mucin 5, subtype B, tracheobronchial	2.9
452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
443959	NM_013409	Hs.9914	SS,kazal	folistatin	2.9
446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
449746	AI688594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-6enC	ESTs	2.9
431628	AU077025	Hs.265827	SS,IRNA_antiSH2,SH3,phkase	interferon, alpha-inducible protein (clon	2.8
445873	AA250970	Hs.251946	SS,rmn,PABPphkase,14-3-3,rmn	poly(A)-binding protein, cytoplasmic 1-II	2.8
438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
410910	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

5	411558	AA102870	Hs.70725	SS,TM	gamma-aminobutyric acid (GABA) A receptor	2.8
	413273	U75679	Hs.75257	TM,lg,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
	433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117	2.7
	452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetical	2.7
	456181	L38463	Hs.1030	TM,RA,VPS9	ras inhibitor	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin	2.7
	422278	AF072873	Hs.114218	TM,Frizzled,Fz	frizzled (Drosophila) homolog 6	2.7
10	446839	BE091926	Hs.16244	TM	mitotic spindle coiled-coil related prote	2.7
	416250	AA581386	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Claudin	hypothetical protein MGC10791	2.7
	407287	AI678812		TM,rascadherin	gbtu59d08.x1 NCLCGAP_Gas4 Homo sapiens	2.7
	412877	AA125910	Hs.191461	TGF-beta	ESTs	2.7
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of t	2.7
15	425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog	2.7
	430152	AB001325	Hs.234642	SS,TM,MIP	aquaporin 3	2.7
	444008	BE395085	Hs.10086	SS,TM	type I transmembrane protein Fn14	2.7
	418869	AW518566		TM,RasGAP,IQ,WW	gbxq01d05.x1 Soares_NHCCc_cervical_tumor	2.7
	416658	U03272	Hs.79432	SS,TM,EGF,TB	fibrillin 2 (congenital contractual aac	2.6
20	410290	AA402307	Hs.322844	SS,TM,Sema,TIG,Plexin_repeat	hypothetical protein DKFZp5564A176	2.8
	419667	AJ077005	Hs.92208	SS,TM,dIntegrin,Reprolysin,Pep_M12B_propep	a disintegrin and metalloproteinase domai	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,TIG,LIM	mal proto-oncogene (hepatocyte growth fac	2.6
	434444	AI765276	Hs.101257	TM	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	TM,ABC_tran,ABC_membrane,Rhomboid	ATP-binding cassette, sub-family C (CFTR)	2.6
25	431890	X17033	Hs.271986	vw,FG-GAP,Integrin_A	Integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	452281	T93500	Hs.28792	TGF-beta,TGFb_propeptide	Homo sapiens cDNA FLJ11041 fls, clone PLA	2.6
	421508	BE302796	Hs.105087	TM,TK	thymidine kinase 1, soluble	2.6
	453331	AI240665	Hs.8895	TM,dIntegrin,Pep_M12B_propep,Reprolysin	ESTs	2.6
	447197	R36076		TM,SDF	gbxh88b01.s1 Soares_placenta Nb2HP Homo	2.6
30	459688	U72671	Hs.151250	SS,TM,lg	intercellular adhesion molecule 5, telom	2.5
	437412	BE069288	Hs.34744	TM,ABC_tran,ABC_membrane,Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.6
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	424420	BE614743	Hs.146688	TM,MAPEG	prostaglandin E synthase	2.5
	427239	BE270447	Hs.174070	TM,UQ_con	ubiquitin carrier protein	2.5
35	407103	AA424881	Hs.256301	TM,cNMP_binding,tryptin	hypothetical protein MGC13170	2.5
	431130	NM_006103	Hs.2719	SS,TM,wrap	epididymis-specific, whey-acidic protein	2.5
	453378	AA035261	Hs.61753	PAN,kiringle,tryptin	ESTs	2.5
	421733	AL119871	Hs.1420	SS,TM,lg,pkinase	fibroblast growth factor receptor 3 (acho	2.5
	452220	BE158006	Hs.212298	TM,Integrin_A,FG-GAP	ESTs	2.5
40	417975	AA641838	Hs.30085	SS,tryptin	hypothetical protein FLJ23186	2.5
	440381	AA817808	Hs.190485	TM	ESTs	2.5
	441794	AW197794	Hs.253338	TM	ESTs	2.5
	439108	AW163034	Hs.6467	SS,TM	synaptogyrin 3	2.5
	401103	NA		TM,vwd	C12001233.gil7305361 ref NP_038652.1 olo	2.4
45	430630	AW269920	Hs.2621	TM,cystatin	cystatin A (stefin A)	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	416821	AI648602	Hs.55468	TM,histone,SacIvagar_tr	ESTs	2.4
	402745			SS,TM,EGF,Iid_recept_Lb,hyroglobulin_1	NM_002508:Homo sapiens nidogen (enactin)	2.4
	407758	D50915	Hs.38365	SS,TM	KIAA0125 gene product	2.4
50	457570	AA579428		TM	gbznf37c09.s1 NCLCGAP_P22 Homo sapiens c	2.4
	429574	BE268321	Hs.208912	SS,TM	hypothetical protein MGC861	2.4
	431211	M88849	Hs.323733	SS,TM,connexin	gap junction protein, beta 2, 26kD (come	2.4
	452885	AI924046	Hs.119567	SS,TM,PMP22_Claudin	ESTs, Weakly similar to A47582 B-cell gro	2.4
	420511	AF052692	Hs.98485	SS,TM,connexin	gap junction protein, beta 3, 31kD (come	2.4
55	437897	AA770661	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	437846	AA773866	Hs.244569	TM	esophagus cancer-related gene-2	2.4
	418432	M14156	Hs.85112	Insulin	insulin-like growth factor 1 (somatomedin	2.3
	438108	AA717395	Hs.287776	TM	vanilloid receptor-related osmotically ac	2.3
	453408	AI192887	Hs.61784	pkinase,Furin-like,Recep_L_domain	hypothetical protein FLJ14451	2.3
60	435542	AA687378	Hs.289533	pkinase,RhoGEF,lg,PH,SH3	ESTs	2.3
	434517	AA635680	Hs.337251	TM	hypothetical protein MGC2487	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,Integrin_A	integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	422310	AA318622	Hs.98370	SS,TM,fn3,lg,pkinase,Ribosomal_L38a,p450	cytochrome P450, subfamily 16, polypepti	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdo48_N	Fanconi anemia, complementation group G	2.3
65	418091	AF295370	Hs.283082	SS,TM,Defensin_beta	defensin, beta 3	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membrane-ns	2.3
	409402	AF208234	Hs.695	TM,cystatin	cystatin B (stefin B)	2.3
	432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
	408243	Y00787	Hs.624	SS,TM,IL8	interleukin 8	2.3
70	423229	AC003966	Hs.125532	SS,tryptin	protease, serine, 26	2.3
	408713	NM_001248	Hs.47042	GDA1_CO39	ectonucleoside triphosphate diphosphohydr	2.3
	440502	AI624113	Hs.78281	RGS,GoLoco,RBD	regulator of G-protein signalling 12	2.3
	429929	AB014593	Hs.226275	TM	KIAA0683 gene product	2.3
	439963	AW247529	Hs.6793	TM,p450Ests	platelet-activating factor acetylhydrolase	2.3
75	428953	AA306610	Hs.194676	SS,TM,TNFR_cf,arf,Statthnin,DEAD	tumor necrosis factor receptor superfamil	2.3
	438398	AA284267	Hs.221504	SS	ESTs	2.2
	440371	BE268560	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
	452203	X57522	Hs.158164	SS,TM,ABC_tran,ABC_membrane	transporter 1, ATP-binding cassette, sub-	2.2
	407811	AW190902	Hs.40098	SS	cysteine knot superfamily 1, BMP antagoni	2.2
80	432078	BE314877	Hs.24553	TM	hypothetical protein FLJ12541 similar to	2.2
	429113	D28235	Hs.196384	SS,TM,EGF	prostaglandin-endoperoxide synthase 2 (pr	2.2
	452755	AW138937	Hs.213438	Glyco_transf_29	ESTs, Weakly similar to A34087 hypothetic	2.2
	428434	AW363580	Hs.65551	SS	Homo sapiens, Similar to DNA segment, Chr	2.2
	429822	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2

	417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfam	2.2
	422012	AW403423	Hs.110746	SS,homoeotax,pou	HCR (a-helix coiled-coil rod homologue)	2.2
	433090	A1720050	Hs.145362	SS,TM	Immortalization-upregulated protein	2.2
5	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransfera	2.2
	409894	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR	5T4 oncofetal trophoblast glycoprotein	2.2
	416763	A1908127	Hs.79748	TM,alpha-amyrase7tm_1	solute carrier family 3 (activators of di	2.2
	425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetical	2.2
10	452799	A1948829	Hs.213786	TM	ESTs	2.2
	414733	BE514535	Hs.77171	TM,MCMHome_oxygenase	minichromosome maintenance deficient (S.	2.2
	448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
	426989	AF120274	Hs.194589	SS	artemin	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,tm	TONDU	2.2
	408308	AL033377	Hs.44187	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
15	408533	AW695943	Hs.21291	TM	mitogen-activated protein kinase kinase k	2.2
	408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
	408996	A1979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
	417900	BE250127	Hs.82906	TM,WD40_pro_isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
20	437191	NM_005846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fls, clone LN	2.1
	431117	AF003522	Hs.250500	SS,TM,DSL,EGF	delta (Drosophila)-like 1	2.1
	447874	BE270640	Hs.19192	TM,ptkinasesar,arf	cyclin-dependent kinase 2	2.1
	408651	H96843	Hs.283565	bZIPcofilin_ADF,EGF	FOS-like antigen-1	2.1
25	440495	AA887212	Hs.14161	TM,NSFNa_Ca_Ex	hypothetical protein DKFZp4341930	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TILA,vwd,EPO_TPO	procollagen C-andopeptidase enhancer	2.1
	421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,lg,MAM	protein tyrosine phosphatase, receptor ty	2.1
	448224	AW995911	Hs.298883	fn3	hypothetical protein FLJ23399	2.1
30	452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
	409956	AW103364	Hs.727	SS,TGF-beta,TGFb_propeptide	inhibin, beta A (activin A, activin AB al	2.1
	438580	AA811262	Hs.298202	TM,ptkinasesugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
	424865	A1956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
35	412270	AC005282	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
	428471	X57348	Hs.184510	TM,14-3-3	stratillin	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprolysin	metallocarboxypeptidase CPX-1	2.1
	416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
	423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
40	417944	AU077198	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
	424197	AF095834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
	446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
	417331	AW411297	Hs.81972	TM,SH2,PI0	SHC (Src homology 2 domain-containing) tr	2.1
	430413	AW842182	Hs.241392	IL8,FX	small inducible cytokine A5 (RANTES)	2.1
45	421885	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting, type 2C, member	2.1
	407305	AA715284	Hs.106778	TM,ptkinase,Sema,Plaxin_repeat,TIG,LIM	gbmv3503,r1 NCL_CGAP_Br5 Homo sapiens c	2.1
	407792	A1077715	Hs.39384	SS	putative secreted ligand homologous to fl	2.0
	418895	AA447014	Hs.193281	SS	hypothetical protein MGC2991	2.0
50	439738	BE246502	Hs.9598	TM,RasGAP,IQ,VW	sema domain, immunoglobulin domain (lg),	2.0
	433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	446872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
	419726	U50330	Hs.1274	SS,TM,Astachn,CUB,EGF	bone morphogenetic protein 1	2.0
	410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
55	426500	NM_014638	Hs.170158	TM	KIAA0450 gene product	2.0
	452194	A1684413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
	425855	AF135025	Hs.169679	SS,trypsin	kallikrein 12	2.0
	434346	AA630445	Hs.116773	TM,Fenfo_reduct	ESTs	2.0
60	426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamily	2.0
	440008	AW051893	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
	424634	NM_003613	Hs.151407	ig_tap_1	cartilage intermediate layer protein, nuc	2.0
	446841	AL049229	Hs.15787	TM,ptkinase,tm	Homo sapiens mRNA; cDNA DKFZp554O1016 (fr	2.0
	418851	A1417828	Hs.192435	TM	ESTs	2.0
65	440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_term	RAD1 (S. pombe) homolog	2.0
	439498	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	454197	BE440988		TM,Ammonium_transphosphatase,Ammonium_transp	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	433573	AF234867	Hs.57652	TM,7tm_2,GPSIRNA-synt_2b,Sary_LIRNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
	428211	AF052683	Hs.198248	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
70	420797	L08098	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamily	2.0
	455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
	414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
	435636	AW292532	Hs.250176	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
	411789	AF245505	Hs.72157	TM,lg,LRRCT	DKFZp5641922 protein	2.0
	441455	AJ271671	Hs.7854	TM,ras,DENN	zinc/iron regulated transporter-like	2.0
75	426068	AF029778	Hs.186154	SS,TM,DSL,EGF,NUDIX	Jagged 2	2.0
	439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROIMAGE 17593	2.0
	435014	BE660898	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
	457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
80	422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
	431104	AW970859	Hs.313503	Sema,lg	ESTs	1.9
	432210	A1587421	Hs.273330	TM,laminin_G,laminin_EGF,kazalubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	436511	AA721252	Hs.291502	TM,disintegrin,Reprolysin,Pep_M128_propep,ptkinase,	ESTs	1.9
	419218	AU076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

5	432169	Y00971	Hs.2810	TM,Pribosyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
	441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetical	1.9
	447160	AA330310	Hs.24181	TM	ESTs	1.9
	419138	U48508	Hs.89631	TM,RYDR,ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
	457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	cathepsin D (lysosomal aspartyl protease)	1.9
	431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30)	1.9
	428957	NM_003881	Hs.184679	SS,TM,vwa,IGFBP,isp_1	WNT1 inducible signaling pathway protein	1.9
	418546	AA224827		TM,vwa,FG-GAP,Integrin_A	gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens c	1.9
10	400749			SS,TM,ld_recept_a,m3,ld_recept_b	NM_003105*Homo sapiens sortilin-related	1.9
	406369	R38438	Hs.182575	F-protein	solute carrier family 16 (H???) transport	1.9
	422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
	417409	BE272506	Hs.82109	TM,Syndecan	syndecan 1	1.9
	407720	AB037776	Hs.38002	TM,calponin,CH	KIAA1355 protein	1.9
15	418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
	434769	AA648884	Hs.134278	TM,CDP-OH_P_transf,MCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
	421593	NM_017436	Hs.105956	SS,TM	globotrioseylceramide/CD77 synthase; Gb3/	1.9
	426064	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
	404804	NA		TM	Target Exon	1.9
20	422753	AJ928995	Hs.1675	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
	422739	H20106	Hs.119591	SS,ClaLadaptor_s	adaptor-related protein complex 2, sigma	1.9
	433068	NM_006456	Hs.288215	SS,Pribosyltran	slalytransferase	1.9
	419594	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
	428188	M68447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 1 (K polypeptide epiderm	1.9
25	428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
	429592	AB029041	Hs.209646	TM,Phl,RasGAP,NTP_transf_2	KIAA1118 protein	1.9
	431620	AA128109	Hs.284981	ig	2'-5'-oligoadenylate synthetase 2 (69-71	1.9
	424870	W61215	Hs.116651	SS,TM,ig	epithelial V-like antigen 1	1.9
	428373	AJ751656	Hs.183986	SS,ig,Sema	poliovirus receptor-related 2 (herpesviri	1.9
30	453449	W16752	Hs.32981	TM,7tm_1	sema domain, immunoglobulin domain (ig),	1.9
	432304	AA932185	Hs.69297	TM,DnaJ,DnaJ_C,DnaJ	ESTs	1.9
	432673	AB028859	Hs.278605	SS,TM,zf-DHHC	DnaJ (Hsp40) homolog, subfamily B, member	1.9
	416207	NM_014745	Hs.336433	TM,Flexin_repeat,Sema,isp_1	Homo sapiens, clone MGC2908, mRNA, compl	1.9
	408988	AL119844	Hs.49476	SS,laminin_EGF,laminin_N_term	Homo sapiens clone TUA8 Cxi-du-duet regio	1.9
35	417426	NM_002291	Hs.82124	SS,TM,serpin,Marek_A	laminin, beta 1	1.9
	443883	AA114212	Hs.9930	SS,TM	serine (or cysteine) proteinase inhibitor	1.9
	433328	AW298159	Hs.23644	TM,SKL_Sno	ESTs, Weakly similar to S65B24 reverse tr	1.9
	419981	AA897581	Hs.128773	SS,TM,IL8	ESTs	1.8
40	420931	AF044197	Hs.100431	TM,Ribosomal_S17Ribosomal_L13	small inducible cytokine B subfamily (Cys	1.8
	416023	AA932146	Hs.133494	TM,Glyco_hydro_2	Homo sapiens clone TCCGA00164 mRNA seque	1.8
	413644	BE154910	Hs.278793	TM,ABC_tran,ABC_membraneon_trans	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
	449987	AW079749	Hs.184719	SS,sushi	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
	421340	F07783	Hs.1369	SS,TM,Collagen,COL1,TSPN	decay accelerating factor for complement	1.8
	417886	AW067803	Hs.82772	TM,transmembrane4RasGEF,RA	collagen, type XI, alpha 1	1.8
45	430259	BE550182	Hs.127826	TM,SDF	RaLGEF-like protein 3, mouse homolog	1.8
	432998	AA835948	Hs.153307	TM,NA	ESTs	1.8
	431671	NM_016837	Hs.267289	trypsin	polymerase (DNA directed), alpha	1.8
	411773	NM_006799	Hs.72026	SS,TM,Peptidase_M10,hemopexin	protease, serine, 21 (testis)	1.8
	425247	NM_006940	Hs.155324	TM,cn160_TCP1,Sema	matrix metalloproteinase 11 (stromelysin	1.8
50	422976	AL076657	Hs.1800	SS,TM,GATase,OTCase,CPSase_L_chain,Dihydroc	chaperonin containing TCP1, subunit 5 (ep	1.8
	425169	NM_004341	Hs.154868	Ricin_B_lectin	carbamoyl-phosphate synthetase 2, asparta	1.8
	447776	AJ525525	Hs.130181	SS,TM,fusion_gly,Myosin_tailactin_short	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
	426906	AW845183	Hs.172851	TM,Na_Ca_ExCam_acyltransf	arginase, type II	1.8
	408116	AA251393	Hs.289052	SS,TM,UNG	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
55	417847	AJ521658	Hs.7331	TM,ubiquitin,laminin_G,laminin_EGF,kazat	hypothetical protein FLJ22318	1.8
	415781	H08366	Hs.78853	TM,p450	uracil-DNA glycosylase	1.8
	407903	AJ287341	Hs.154029	TM,ion_trans,K_tetra	bHLH factor Hes4	1.8
	422511	AL076442	Hs.117838	TM,asp	collagen, type XVII, alpha 1	1.8
	414117	W88559	Hs.1787	TM,TPR,ptkase,lg,B56	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
60	426841	AJ052358	Hs.193726	TM,sugar_tr,Fork_head	ESTs	1.8
	416272	AA164215	Hs.203188	FGF	ESTs	1.8
	426440	BE382756	Hs.169902	SS,TM,lectin_c	solute carrier family 2 (facilitated gluc	1.8
	419488	AA316241	Hs.90691	SS,NGF	nucleophosmin/nucleoplasm 3	1.8
	418452	BE379749	Hs.85201	SS,TM	C-type (calcium dependent, carbohydrate-r	1.8
65	431363	M86528	Hs.286902	TGF-beta,bZIP	neurotrophin 5 (neurotrophin 4/5)	1.8
	440975	AW499914	Hs.7579	SS	hypothetical protein FLJ10402	1.8
	438962	BE048694		TM,mila_carr,Lysyl_oxidase	gb:nc41c11.x1 NCL_CGAP_RDF2 Homo sapiens	1.8
	414802	AW630088	Hs.76550	TM,Galactosyl_T	Homo sapiens mRNA; cDNA DKFZp564B1264 (fr	1.8
70	418054	NM_002318	Hs.83354	TM	lysyl oxidase-like 2	1.8
	440501	AA887391	Hs.202229	TM	ESTs	1.8
	449309	AW589823	Hs.224188	TM,Lysyl_oxidase,SCP2,Band_7	ESTs	1.8
	421461	AW291023	Hs.97255	TM,lectin_c	ESTs, Weakly similar to A46010 X-linked r	1.8
	412584	X54870	Hs.74085	TM	DNA segment on chromosome 12 (unique) 248	1.8
	441565	AW953575	Hs.303125	TM,7tm_3,ANF_receptor,sushi	p53-induced protein PIGPC1	1.8
75	431837	T79326	Hs.328553	SS,Y_phosphataseTIG	olfactory receptor, family 2, subfamily I	1.8
	436251	BE515065	Hs.296585	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	nucleolar protein (KKEAD repeat)	1.8
	448833	AA311426	Hs.21635	SS,TM,TSPN,Collagen	tubulin, gamma 1	1.8
	424291	AL120051	Hs.144700	TM,LRR,LRRCT	ephrin-B1	1.8
	415388	AF018081	Hs.78409	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	collagen, type XVIII, alpha 1	1.8
80	435550	AJ244656	Hs.4834	SS,TM,trypan	H.sapiens polyA site DNA	1.8
	448568	AA149121	Hs.71947	SS,Stathmin	ESTs	1.8
	439246	AJ498072	Hs.77783		membrane-associated tyrosine- and threonl	1.8
	413001	AB041036	Hs.57771		kalikrein 11	1.8
	417312	AW888411	Hs.81915		leukemia-associated phosphoprotein p18 (s	1.8

5	444152	AI125694	Hs.149305	TM	hypothetical protein MGC2803	1.8
	453454	AW052006	Hs.8551	TM	PRP4/STK/WD splicing factor	1.8
	449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
	428329	AA426091	Hs.98453	TM,Gal-bind,lectin	ESTs, Moderately similar to R27328.2 (Hs)	1.8
	452875	BE275760	Hs.30928	TM,Apolipoproteinlg	DNA segment on chromosome 19 (unique) 117	1.8
	444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
	443534	AI078123		TM	glyoxylate04.x1 Soares_fetal_liver_spleen_1	1.8
	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-tRNA synthetase	1.8
10	452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
	453140	AA032238	Hs.170531	TM	ESTs	1.8
	418641	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domain	1.8
	432925	AA878324	Hs.192734	SS	ESTs	1.8
	453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
15	457663	AW371946	Hs.337459	TM	ESTs	1.8
	452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
	436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site fam1	1.8
	452635	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
	459647	R34107	Hs.198287	ig	pregnancy specific beta-1-glycoprotein 11	1.7
20	418245	AA088767	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
	448484	BE613940	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
	431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
	434877	AW974792	Hs.292171	TM	ESTs	1.7
	428923	BE047698	Hs.188786	TM	ESTs	1.7
25	402915	NA		TM,HCO3_cotransp	ENSP00000202587-Bicarbonate transporter	1.7
	420185	AL044056	Hs.158047	TM	ESTs	1.7
	445739	AW138354	Hs.145303	TM	ESTs	1.7
	409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
	408688	AI634522	Hs.152926	TM	KIAA1268 protein	1.7
30	420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
	433933	AI754389	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.7
	430965	AA889732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	ESTs	1.7
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_YDP	ATPase, Na ⁺ transporting, beta 3 polypept	1.7
	423484	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
35	416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_tr,PDZ_LIM	LIM domain protein	1.7
	409012	AL117435	Hs.49725	TM,RhoGEFzf-DHHC,adh_short	DKFZP434I216 protein	1.7
	423804	AW403448	Hs.1705	TM,IRF	Interferon-stimulated transcription facto	1.7
	410418	D31382	Hs.53325	SS,TM,trypsin_ML_recept_a	transmembrane protease, serine 4	1.7
	440028	AW473675	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetic	1.7
40	457646	AA725850	Hs.112948	TM,SPRY	ESTs	1.7
	445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
	420426	AA262046	Hs.36567	TM,Galactosyl_T_2ATP-symLC	Homo sapiens cDNA FLJ14227 fls, clone NT2	1.7
	431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit	1.7
	412338	AA151527	Hs.69485	TM,Sama,Plaxin_repeatTIG,Plaxin_repeat	hypothetical protein FLJ12436	1.7
45	414799	AI752416	Hs.77326	SS,thyroglobulin_t,IGFBP	insulin-like growth factor binding protei	1.7
	452700	AI859390	Hs.288940	TM,DIX,RGS,thiorel	five-span transmembrane protein M83	1.7
	430877	NM_005269	Hs.2689	GST_C,tRNA-synt_1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
	428624	AI125222	Hs.98712	TM,thiorel,Y_phosphatase,MAM,lg,fn3MSP_domain	hypothetical protein DKFZp434H0311	1.7
	444065	AW449415	Hs.10260	TM,Ion_trans	Homo sapiens cDNA FLJ11341 fls, clone PLA	1.7
50	416319	AI815801	Hs.79197	SS,TM,lg	CD83 antigen (activated B lymphocytes, im	1.7
	429367	AB007867	Hs.278311	Sama,Plaxin_repeat,TIG	plaxin B1	1.7
	430425	AA531428	Hs.241412	TM	apolipoprotein L_2	1.7
	441668	AB11973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
	418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
55	450835	BE262773	Hs.25584	TM,AncGap	hypothetical protein FLJ10767	1.7
	418859	AA229558		TM	glucosylase10.s1 NCL CGAP_P11 Homo sapiens c	1.7
	425304	AA453844	Hs.31339	TM,lg,ITAM	fibroblast growth factor 11	1.7
	423635	X85019	Hs.130181	TM,Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.7
	414820	AA371931	Hs.77422	TM,Ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
60	440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
	412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
	422087	X58968	Hs.111301	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
	407151	H26836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown (Hsa	1.7
	410726	AI823859	Hs.15936	TM,PX	ESTs	1.7
65	452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	Homo sapiens cDNA: FLJ22993 fls, clone KA	1.7
	409220	BE243323	Hs.51239	TM,death,TNFR_c6	tumor necrosis factor receptor superfamily	1.7
	427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
	426410	BE288446	Hs.305890	TM,Bcl-2,BH4	BCL2-like 1	1.7
70	433598	AI762636	Hs.271433	TM,Cytidylyltransf,SIR27tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
	436495	BE258949	Hs.290874	TM,Armadillo_seg	ESTs, Weakly similar to ALU8_HUMAN ALU 8U	1.7
	422032	AA476966	Hs.110867	TM,TFIS,RNA_POL_M_15KDsarlin,hormone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
	429736	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamily	1.7
	427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
75	431981	AA684069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
	407738	NA1744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
	420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankyrin r	1.7
	424620	AA101043	Hs.161254	SS,TM,trypsin	kallikrein 7 (chymotryptic, stratum come	1.7
	430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
80	423393	R37772	Hs.21420	TM,thiorelphkinase	p21-activated protein kinase 6	1.7
	444051	N48373	Hs.10247	SS,lg		

TABLE 13B

5	Pkey:	Uniqua Eos probaset identifier number	
	CAT number:	Gene cluster number	
10	Accession:	Genbank accession numbers	
	Pkey	CAT Number	Accessions
15	408344	105240_1	AA053843 BE162213
	418546	176677_1	AA224827 T59708 T59843 BE158903
	418659	179717_1	AA229558 AA345492 AA229582
	418669	179863_1	AW516565 AA229762 AA230035
20	437938	44573_2	AW516565 AA229762 AA230035
			A1950087 N70208 R87040 N36809 A1308119 AW967677 N35320 A1251473 H59397 AW971573 R97278 W01059 AW967671 AA808598 AA251875
			A1820501 A1820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 A1219788 AA884444 N92578 F13493
			AA927794 A1560251 AW874068 AL134043 AW235383 AA663345 AW008282 AA488964 AA283144 A1890387 A1950344 A1741346 A1669062
25			AA262915 AW102898 A1872183 A1763273 AW173586 AW150329 A1663832 A1762688 AA988777 AA488892 A1366394 AW103613 A1539642
			AA642789 AA856975 AW505512 A1961530 AW629970 BE612861 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499
			AW961101 AA251669 AA251874 A1819225 AW205862 A1683336 A1856509 AW276905 A1633006 AA972584 AA508741 AW072629 AW513696
			AA293273 AA969759 N76628 N22386 H84729 H80052 T92467 A1022058 AA780418 AA551005 W80701 AW613456 A1373032 A1564289 F00631
30			H83488 W37181 W78802 R66056 A1002839 R67840 AA300207 AW959581 T63226 F04005
	438952	467390_1	BE046594 BE046667 AA828585 A1207343
	443634	572957_1	A1076123 A1244834 A1695239
	447197	711623_1	R36075 A1366546 R36167
35	454197	1050392_1	BE140968 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969
			BE141673 BE141650 BE141674 BE141650 BE141688 AW178241 BE140994 BE141666 BE140988 BE141008 BE140988 BE141011 BE140975
			BE141667 BE141676 BE141657 BE141681 BE141656 BE141672 BE141660 AW178237 BE141012 BE140890 BE141658 BE141648 BE141013
			BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646
40			BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671
			AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141656
	455333	1281044_1	AW897851 AW897852
	457570	357443_1	AA579426 AA579438 AA573736

TABLE 13C

40	Pkey:	Unique number corresponding to an Eos probaset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1993) 402:489-495.	
45	Strand:	Indicates DNA strand from which exons were predicted.	
	Nt_position:	Indicates nucleotide positions of predicted exons.	
50	Pkey	Ref	Strand
	400666	8118496	Plus
55	400749	7331445	Minus
	401103	8568122	Minus
60	401486	7341763	Plus
	401575	7229804	Minus
65	402745	9212200	Minus
	402915	7406502	Minus
70	404440	7528051	Plus
	404604	9212537	Minus
75	405545	1054740	Plus
	405547	1054740	Plus
80	406400	9256298	Plus
	406467	9795551	Plus

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modifiable by small molecules (e.g. kinase, peptidase, phosphatase, ATPase, or ion transporter domains). The predicted protein domains are noted.

70	Pkey:	Unique Eos probaset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
75	UnigenetID:	Unigene number			
	PPDomains:	Predicted Protein Domains			
80	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal adult tissues			
	Pkey	ExAccn	UnigenetID	PPDomains	R1
	418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interst
	439506	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87
	400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stroma
	415817	U88967	Hs.78867	SS,TM,Y_phosphatase,carb_anhyd	protein tyrosine phosphatase, recep
	416209	AA235778	Hs.79078	TM,HORMA	MAO2 (mitotic arrest deficient, yea
	404996	NM_001333	Hs.87417	Peptidase_C1	CTSL2 Cathepsin L2

	429518	AA885360	His.160199	phkase	Target CAT	12.7
	429486	AF155827	His.203963	helicase_C,SNF2_Nhelicase_C	hypothetical protein FLJ10339	12.6
	419183	U60669	His.83663	p450	cytochrome P450, subfamily XXIV (vi	12.3
5	428368	BE440042	His.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromal	10.2
	420759	T11832	His.127797	helicase_C	Homo sapiens cDNA FLJ11381 fls, clo	10.2
	458194	AW383618	His.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
	446232	AI281848	His.194691	TM,7tm_3Ribosomal_L13	retinoid acid induced 3	8.9
	424905	NM_002497	His.153704	TM,phkase	NIMA (never in mitosis gene a)-rela	8.9
10	452291	AF015582	His.26853	TM,phkase	CDC7 (cell division cycle 7, S. cer	8.7
	424086	AI351010	His.102267	Lysyl oxidase	lysyl oxidase	8.3
	425710	AF030880	His.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
	433133	AB027249	His.104741	TM,Collagen,phkase	PDZ-binding kinase; T-cell originat	7.4
	447254	NM_004153	His.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1
15	431941	AK000106	His.272227	phkase,Furin-like,Recap_L_dom	Homo sapiens cDNA FLJ20089 fls, clo	6.9
	427821	AA470158	His.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	His.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
	403471	NA		SS,TM,tryptin	Target Exon	6.7
	410153	BE311826	His.15830	Glycos_transf_2	hypothetical protein FLJ12681	6.6
20	457405	AA504860		TM,7tm_2	gbxab03a10.s1 Stratagene fetal reti	6.4
	421948	L42583	His.334309	filament,HC03_cotranspfilament	keratin 6A	6.3
	439292	AA090421	His.5555	TM,AAA,Ferri_reduct	hypothetical protein MGC5347	5.8
	413625	AW451103	His.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
	425695	NM_005401	His.159238	TM,Band_41,Y_phosphatase	protein tyrosine phosphatase, non-r	5.7
25	438394	BE378623	His.27693	SS,pro_isomerase	peptidylprolyl isomerase (cytophil	5.6
	432239	X81334	His.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
	408536	AW381532	His.135188	SS,TM,E1-E2_ATPase,Cation_ATPA	ESTs	5.4
	432226	AW182766	His.273558	Cytidyltransfer	phosphate cytidyltransferase 1, c	5.2
	419620	AB009303	His.50800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
30	426360	NM_003245	His.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
	421155	HI87879	His.102267	SS,Lysyl_oxidase,Aldose_eplm,E	lysyl oxidase	4.9
	423673	BE003054	His.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
	450375	AA009647	His.8850	TM,disintegrin,Pept_M12B_propep	a disintegrin and metalloproteinase	4.8
	418379	AA218940	His.137516	AAA	fdgetin-like 1	4.7
35	457465	AW301344	His.122808	Phibosyltran,Sulfatase	DNA replication factor	4.6
	412333	AW937485		TM,7tm_1	gbxQV3-DT0044-221299-045-b09 DT0044	4.6
	450510	AA010066	His.242998	DNA_topoisomII,DNA_topoisomVGF	ESTs	4.6
	436291	BE568452	His.5101	abhydrolase	protein regulator of cytokinesis 1	4.6
	448353	AI290919	His.459661	HECTphkase	ESTs	4.5
40	435435	T89473	His.192328	lipase,PLAT	ESTs	4.5
	425071	NM_013989	His.154424	SS,TM,T4_deiodinase	deiodinase, lodothyronine, type II	4.4
	433322	H50621	His.134156	TM,Ion_transNB-ARC,CARD,milo,c	ESTs, Weakly similar to I38022 hypo	4.4
	408808	BE296227	His.260822	TM,phkase	serine/threonine kinase 15	4.4
	444781	NM_014400	His.11950	PH,lactamase_B	GPI-anchored metastasis-associated	4.4
45	428479	Y00272	His.184572	phkase	cell division cycle 2, G1 to S and	4.2
	408687	M31126	His.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
	423035	AW449679	His.156739	TM,Glyco_transf_B	H.sapiens XG mRNA (clone PEP11)	4.2
	449228	AJ403107	His.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	423738	AB002134	His.132195	SS,TM,tryptin,SEA	airway trypsin-like protease	4.1
50	457030	AI301740	His.173381	TM,Dihydroorotase	dihydropyrimidine-like 2	4.1
	448895	AI613276	His.5582	adenylatekinase	guanine nucleotide binding protein	4.0
	415857	AA866115	His.127797	helicase_C	Homo sapiens cDNA FLJ11381 fls, clo	4.0
	438390	AA22017		TM,DSL,7tm_17tm_1	gbx45f12.x1 NCL_CGAP_Bm23 Homo s	4.0
	429900	AA450421	His.30875	phkase	ESTs	4.0
55	446292	AF081487	His.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	422938	NM_001809	His.1594	TM,thiolase	centromere protein A (17kD)	3.7
	408771	AW732573	His.47584	TM,K_tetra,lon_trans	potassium voltage-gated channel, de	3.6
	424286	AK31874	His.155140	phkase	casein kinase 2, alpha 1 polypeptid	3.6
	436246	AW450863	His.119591	connexinhormone_rec,zf-C4	ESTs	3.5
60	411274	NM_002776	His.89423	tryptin	kallikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425dHomo sapiens matrix metal	3.5
	426820	AA393351	His.132121	PDEase	ESTs	3.5
	412471	MB3193	His.73946	SS,TM,Glycos_transf_3,Cam_acy	endothelial cell growth factor 1 (p	3.4
	430704	AW813091	His.335799	Epimerase	ESTs	3.4
65	455092	BE152428		Sulfatase	gbxCMO-HT0323-151299-128-b04 HT0323	3.4
	453775	NM_002916	His.38120	AAA,PI3_PI4_kinase,PI3Ka,PI3K_	replication factor C (activator 1)	3.4
	438993	AA828995		Integrin_B	gbxod77b08.s1 NCL_CGAP_Ov2 Homo sap	3.4
	426572	AB037783	His.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
	449101	AA205847	His.23018	SS,TM,7tm_1	G protein-coupled receptor	3.3
70	427880	AI741320	His.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fls, cl	3.3
	402481			TM,GDI,7tm_1	NM_001621~Homo sapiens choroiderem	3.3
	414774	X02419	His.77274	SS,kringle,tryptin	plasminogen activator, urokinase	3.3
	412246	AI160873	His.58233	SulfotransferaseCOX	zinc finger protein	3.3
	418462	BE001596	His.85266	SS,TM,Integrin_B,fn3	integrin, beta 4	3.3
75	424687	J05070	His.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatin	3.3
	401486	NA		SS,TM,tryptin	C4000647~gll4758508jreflNP_004253.	3.2
	408113	T82427	His.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fls, cl	3.2
	427359	AW020782	His.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fls, cl	3.2
80	402337			SS,p450	Target Exon	3.2
	420930	AW888850		ribonuclease_T2	gbxCM4-NT0007-130500-551-f08 NT0007	3.2
	443426	AF088158	His.8329	phkase	chromosome 20 open reading frame 1	3.1
	439760	AL359053	His.57664	TM,Integrin_B,Ricin_B_lectin	Homo sapiens mRNA full length inser	3.1
	420039	NM_004605	His.94581	CARD,SulfotransferaseDAGKc	sulfotransferase family, cytosolic,	3.0
	448733	NM_005629	His.187958	SS,TM,SNF,ABC_tran,Isodh,phkna	solute carrier family 6 (neurotrans	3.0

444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
450841	A741466	Hs.270515	pro_isomerase	ESTs	3.0
428262	AI651324	Hs.7298	death_pkinase	blphenyl hydrolase-like (serine hyd	3.0
435399	AA679463		pklnase	gbac50c03.s1 Stratagene hNT neuron	2.9
446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
449746	AI668594	Hs.176568	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
414581	AA256213	Hs.72010	TM,Carn_acyltransf,Choline_kin	ESTs	2.9
431629	AU077025	Hs.265827	SS,IRNA_antISH2,SH3,pkinase	interferon, alpha-inducible protein	2.8
445873	AA250970	Hs.251946	SS,rm,PABPpkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic	2.8
438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
422689	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
439453	BE264974	Hs.6566	SS,AAA	thyroid hormone receptor interactor	2.8
413582	AW295847	Hs.71331	carb_anhydase	hypothetical protein MGC5350	2.8
410684	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
458456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
413273	U75679	Hs.75257	TM,lg,pkinase	stem-loop (histone) binding protein	2.8
426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0035 gene product	2.8
403763			TM,7tm_1	NM_001059:Homo sapiens tachykinin	2.7
408360	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
401230			SS,TM,lon_trans,IQ	NM_014191:Homo sapiens sodium chan	2.7
418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
445640	AW569526	Hs.31704	TM,alpha-amyrase	ESTs, Weakly similar to KIAA0227 [H]	2.7
432865	A1753709	Hs.152484	TM,lon_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I3022 hypo	2.6
419667	ALU077005	Hs.92208	SS,TM,disintegrin,Reprolysin,P	a disintegrin and metalloproteinase	2.6
406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,	met proto-oncogene (hepatocyte grow	2.6
412530	AA766268	Hs.266273	abhydrolase	hypothetical protein FLJ13346	2.6
431890	X17033	Hs.271986	vwa,FG-GAP,Integrin_A	Integrin, alpha 2 (CD49B, alpha 2 s	2.6
404184	NA		SS,TM,7tm_1	NM_030903:Homo sapiens olfactory r	2.6
428450	NM_014791	Hs.184339	pklnase,KA1	KIAA0175 gene product	2.6
425898	NM_016112	Hs.159241	TM,pkinase,lon_trans	polycystic kidney disease 2-like 1	2.6
453331	A1240665	Hs.8695	TM,disintegrin,Pepp_M12B_propap	ESTs	2.6
444826	AI674482	Hs.148441	pklnase,SAM	ESTs	2.6
414987	AA524394	Hs.294022	connexin43hormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
438746	AI858315	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.6
429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
421733	AL115671	Hs.1420	SS,TM,lg,pkinase	fibroblast growth factor receptor 3	2.5
452220	BE158006	Hs.212296	TM,Integrin_A,FG-GAP	ESTs	2.5
417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
400301	X03635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
411643	AI924519	Hs.192570	DEAD,helicase_C	hypothetical protein FLJ22028	2.4
446638	AL133063	Hs.15783	TM,pkinase	Homo sapiens mRNA: cDNA DKFZp434P11	2.4
430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
417855	AA780791	Hs.14014	Peptidase_M41,AAApklnase	hypothetical protein FLJ14813	2.4
448005	AW207437	Hs.170378	pklnase	ESTs	2.4
423973	AF033461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R I	2.4
437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
425397	J04088	Hs.156348	DNA_topoisolI,DNA_topoisolVIGF	topoisomerase (DNA) II alpha (170kd	2.4
432777	AA564991	Hs.269477	alpha-amyrase	ESTs	2.4
421247	BE391727	Hs.102910	TM,IRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIB, p	2.4
425485	L18964	Hs.1904	TM,pkinase,DAG_PE-bind,OPR,pkl	protein kinase C, iota	2.4
419281	H98452	Hs.42189	TM,E1-E2_ATPase,HMA,Hydrolase	ESTs	2.4
434205	AF118851	Hs.283032	SH3,efhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
453406	AI192987	Hs.61784	pklnase,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
435542	AA687378	Hs.269533	pklnase,RhoGEF,lg,PH,SH3	ESTs	2.3
443151	AI827193	Hs.132714	DNA_mis_repair,HATPase_cAcylph	ESTs	2.3
431630	NM_002204	Hs.265829	SS,TM,FG-GAP,Integrin_A	Integrin, alpha 3 (antigen CD48C, a	2.3
422310	AA316622	Hs.98370	SS,TM,fn3,lg,pkinase,Ribosomal	cytochrome P450, subfamily IIS, pol	2.3
441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation gro	2.3
414907	X90725	Hs.77597	SS,TM,pkinase,PCLO_box	polo (Drosophila)-like kinase	2.3
439810	AL109710	Hs.86658	aconitase,Aconitase_C	EST	2.3
429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
452947	AW130413		alpha-amyrase	gbad50f04.x1 NCL_CGAP_Gas4 Homo sa	2.3
423229	AC003865	Hs.125532	SS,trypsin	protease, serine, 26	2.3
453941	U89817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhy	2.3
424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
452765	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
434149	Z43829	Hs.19574	TM,EPH_lbd,fn3,pkinase,SAM	hypothetical protein MGC5469	2.2
417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
416763	AI908127	Hs.79748	TM,alpha-amyrase7tm_1	solute carrier family 3 (activators	2.2
414733	BE514535	Hs.77171	TM,MCM/heme_oxygenase	minichromosome maintenance deficien	2.2
443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
452367	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

5	424490	AJ278016	Hs.55565	TM, pkinase, ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM, 7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N, helicase_C	RAD54 (S.cerevisiae)-like	2.1
	418804	AA809632		HATPase_c, HSP90, PHD, zf-C2H2	gbnz17h04.s1 NCL CGAP_GCB1 Homo sa	2.1
	447674	BE270640	Hs.19192	TM, pkinase, arf	cyclin-dependent kinase 2	2.1
	450663	H43540	Hs.25292	SS, TM, RNase_HII	ribonuclease HI, large subunit	2.1
	408805	H69912	Hs.48269	TM, pkinase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS, CUB, NTR, MAM, TIL, TILa, ywd, EP	procollagen C-endopeptidase enhance	2.1
10	447827	U73727	Hs.19718	SS, TM, Y_phosphatase, fn3, ig, MAM	protein tyrosine phosphatase, recep	2.1
	428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS, TM, pkinase, fn3	NM_002944*Homo sapiens v-ros avian	2.1
	403133			pklnase_K_tetra, Band_41, RhoGEF	Target Exon	2.1
	440249	AI246590	Hs.337275	VHL, TalD_DNase	ESTs	2.1
15	438580	AA811262	Hs.299202	TM, pkinase, sugar_tr	ESTs	2.1
	406400			SS, TM, trypsin	NM_007198*Homo sapiens kallikrein 8	2.1
	427375	AL035460	Hs.177536	SS, Zn_carbOpept, hormone5Rprol	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS, Granin, CDP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
20	420757	X78592	Hs.99915	TM, hormone_rec, Androgen_recep,	androgen receptor (dihydrotestoster	2.1
	425018	BE245277	Hs.154185	DNase_I, K_tetra	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM, E1-E2_ATPase, HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_isomerase	ESTs	2.1
	407305	AA715284		TM, pkinase, Sema, Plexin_repeat,	gb:mv35f03.r1 NCL CGAP_fx5 Homo sap	2.1
25	456327	H68741	Hs.38774	TM, Glyco_transf_B	ESTs	2.0
	422429	AA310527		pklnase, RGS, Phklnase, PH, RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRHhormone5, hormone4	gonadotropin-releasing hormone 2	2.0
	458016	AW188099	Hs.131813	pklnase	ESTs	2.0
	452194	AJ694413	Hs.332849	TM, 7tm_3, ANF_receptor, sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182018	TM, pkinase, MBD	Interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	pklnase, lipoxygenase, PLATlipo	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM, DEAD, helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W80363	Hs.58446	pklnase, Furin-like, Recep_L_dom	ESTs	2.0
	418140	BE613836	Hs.83551	TM, E1-E2_ATPase	microtubule-associated protein 2	2.0
35	430076	AA485115	Hs.318773	AAA, BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.158448	Ribosomal_L7Ae, LRR, LRRCT, pklna	surfeit 2	2.0
	425855	AF135025	Hs.159679	SS, trypsin	kallikrein 12	2.0
	400135	L40027	Hs.118890	pklnase	glycogen synthase kinase 3 alpha	2.0

40 TABLE 14B

Pkey: Unique Eos probaset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

45	Pkey	CAT number	Accessions
50	412333	1289037_1	AW937485 AW937589 AW937658 AW937664 AW937492
	418804	179138_1	AA808632 AJ817245 AJ701732 AA228406
	420330	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
	422429	218469_1	AA310527 AW982295 Z44865 H06641
	422669	218886_1	AW856665 AA315006 AW954733
	435399	405576_1	AA679463 AW813779 AW813709
55	438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI325592 AM20795 AI208187 AI423279 AI423645 AI424090 AI359637 ALD44732 D17003
	438993	467651_1	AA828995 AA834879 AI926361
	452947	939810_1	AW130413 AI932362
	455092	1252971_1	BE152428 AW855572 AW855607
	457405	333127_1	AA504860 AA504911

60 TABLE 14C

Pkey: Unique number corresponding to an Eos probaset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	Nt_position
	400686	8118496	Plus	17982-18115, 20297-20456
	401230	9929527	Minus	33835-34006, 34539-34592, 36461-36745, 48925-49096, 52604-52758
	401486	7341763	Plus	32585-32756, 35281-36540, 40791-40933, 44018-44179
75	402337	6957691	Plus	4116-4288, 16811-16973, 17107-17258, 19715-20040, 22029-22205
	402481	9797406	Plus	87891-88891
	403133	7331427	Plus	38314-38634
	403471	9930669	Minus	85867-85983
	403763	7229888	Minus	43575-43887
80	404184	4581418	Minus	12652-13549
	404274	9885189	Plus	104127-104318
	406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

5 Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 96th percentile value amongst cervical cancers was greater than or equal 80 units.

10 Pkey: Unique Eos probaset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	414916	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
	421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
20	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
	454390	AB020713	Hs.56966	KIAA0906 protein	30.5
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
	433226	AW503733	Hs.9414	KIAA1488 protein	30.0
	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
25	411889	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
	414132	AI801235	Hs.48480	ESTs	28.3
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
	448589	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
30	418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
	449722	BE280074	Hs.23960	cyclin B1	26.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
35	432817	NM_014125	Hs.279612	PRO0327 protein	24.6
	412630	AA768268	Hs.266273	hypothetical protein FLJ13346	23.6
	457465	AW301344	Hs.122908	DNA replication factor	23.1
	408808	AW647814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
	429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
40	401405			Target Exon	22.8
	426272	AW450671	Hs.169284	ESTs	22.7
	424878	H57111	Hs.221132	ESTs	22.6
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rakinesin 6)	22.5
	444371	BE540274	Hs.239	forkhead box M1	22.2
45	418030	BE207573	Hs.63321	neuromedin B	22.0
	452291	AF015692	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
	400196			Eos Control	21.3
	416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
50	424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
	438011	BE486178	Hs.145696	splicing factor (CC1.3)	20.7
	426366	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
	436923	AW293704	Hs.122658	ESTs	20.2
	415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
55	448775	AB026237	Hs.388	nucleoside diphosphate linked moiety X)-type m	19.6
	435647	AI853240	Hs.49823	ESTs	19.6
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
	428486	AF165827	Hs.203963	hypothetical protein FLJ10339	19.5
	428433	AA521410	Hs.41371	ESTs	19.4
60	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
	417308	H60720	Hs.81892	KIAA0101 gene product	19.2
	429674	BE268321	Hs.208912	hypothetical protein MGC861	19.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
65	438899	AF085633	Hs.135624	ESTs	19.0
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
	408908	BE286227	Hs.250822	serine/threonine kinase 15	18.8
	427488	M81401	Hs.176658	RAD23 (S. cerevisiae) homolog B	18.6
70	400195			NM_007057*Homo sapiens ZW10 Interactor (ZWINT), tran	18.5
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	18.4
	410324	AW292539	Hs.30177	ESTs	18.3
	453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
	410608	AI638438	Hs.159087	ESTs	18.1
	432503	AA551196	Hs.188952	ESTs	17.9
75	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM5	17.7
	430709	R34356		gbyh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
	449962	AA004879	Hs.187820	ESTs	17.3
	425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
	440774	AI420611	Hs.127832	ESTs	16.8
80	408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [16.7
	426897	AW976570	Hs.97387	ESTs	16.5
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

5	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AF539516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
	453941	U39817	Hs.36820	Bloom syndrome	16.1
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
	407999	AF125271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fls, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
10	425318	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
	423673	BE003054	Hs.1696	matrix metalloproteinase 12 (macrophage elastase)	15.5
	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AF583187	Hs.9700	cyclin E1	15.2
15	407786	AA687538	Hs.38972	telraspan 1	15.2
	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.2
	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432892	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.1
20	427999	AF435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	15.0
	431829	AU070725	Hs.265827	Interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	435354	AA578267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
25	418109	AA203311	Hs.126550	suppressor of K transport defect 1	14.8
	417933	X02308	Hs.82962	thymidylate synthetase	14.7
	438970	AA837782	Hs.321058	ESTs	14.7
	409580	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
30	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420784	AW972872	Hs.293736	ESTs	14.5
	434256	AF378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960573	Hs.177530	ATP synthase, H transporting, mitochondrial F1 comple	14.3
35	427081	AF474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN III ALU CLASS	14.2
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY GC S	14.2
	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391804	Hs.62861	guanylate binding protein 1, Interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
40	418803	U60079	Hs.88556	histone deacetylase 1	14.0
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	14.0
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	AF274270	Hs.96840	KIAA1527 protein	13.9
45	431838	AF097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
	404630			Target Exon	13.6
50	408321	AW405882	Hs.44205	cortistatin	13.6
	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219*gl[12737280]refXP_006682.2 keratin 18 [H	13.5
55	458614	AV653110	Hs.108650	hypothetical protein FLJ20539	13.5
	425281	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
	439926	AW014875	Hs.137007	ESTs	13.3
	411283	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
60	447390	X96384	Hs.18428	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109280A B cell growth factor	13.2
	410068	AF633888	Hs.58435	FYN-binding protein (FYN-120/130)	13.1
	407596	BE350012	Hs.248365	ESTs	13.1
65	432721	AF121478	Hs.180532	glucose phosphate isomerase	13.1
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte associ	13.0
	413314	BE081565		gb:QV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	13.0
	430929	AA489165	Hs.166933	ESTs	12.9
	449571	AW016812	Hs.200286	ESTs	12.9
70	400298	AA032279	Hs.81635	six transmembrane epithelial antigen of the prostate	12.8
	417105	X60982	Hs.81226	CD6 antigen	12.6
	434263	N34885	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferritin associate	12.6
	407756	AA116021	Hs.38280	ubiquitin specific protease 18	12.5
75	437058	AF147081		gb:ok33a1.1.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	12.5
	438768	AF307418	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AA010907	Hs.184455	hypothetical protein	12.4
	418205	L21715	Hs.83760	tropomyosin I, skeletal, fast	12.4
	442994	AF026718	Hs.16954	ESTs	12.4
80	433901	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fls, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S85657 alpha-1C-adrenergic re	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylgl	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

5	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
	432325	AW973209	Hs.261782	ESTs	12.3
	414761	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LING00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
	415443	T07363	Hs.7948	ESTs	12.1
	429770	AF766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
15	432810	AA863400	Hs.23054	ESTs	12.1
	434423	NM_006769	Hs.3844	LM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	458273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
25	434408	AJ031771	Hs.132586	ESTs	11.8
	406747	AJ925153	Hs.217493	annexin A2	11.8
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	446865	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427627	AJ809057	Hs.302083	immunoglobulin heavy constant mu	11.7
	432287	AJ001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.58009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
35	409931	BE293233	Hs.129771	ESTs	11.4
	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
40	433849	BE455884	Hs.280728	ESTs	11.4
	430519	AF129534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AJ905780	Hs.198272	Target CAT	11.3
	422713	AA502780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW498885	Hs.9456	SWWSNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	418741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AJ686945	Hs.272062	ESTs	11.2
	446849	AJ076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 573057B08 gene,	11.2
50	442737	AB002319	Hs.8663	KIAA0321 protein	11.2
	409113	AA074897		gbczmB5a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA168345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402639	AW502781	Hs.30609	KIAA0430 gene product	11.0
55	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
	414706	AW340125	Hs.76989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.236832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J 5E	11.0
	438995	AJ277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.22558	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gbczm76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	H85689	Hs.225580	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AJ393122	Hs.134726	ESTs	10.9
	444655	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
65	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
	400090			Eos Control	10.8
	424517	AJ539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	448099	T93096	Hs.17125	hypothetical protein MGC15912	10.7
70	451056	AJ768660	Hs.206132	ESTs	10.7
	408235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [10.7
	451730	AF085687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AJ948668	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
75	439854	AJ005270	Hs.123543	ESTs	10.6
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AJ815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AJ056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vacuolin related kinase 2	10.6
80	439975	AW328081	Hs.6817	Inosine triphosphatase (nucleoside triphosphatase pyrop	10.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC B	10.5

5	416584	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fls, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fls, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
	410146	AW592655		gb:bf45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 {	10.4
10	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial collagenase)	10.4
	407241	M34516		gb:Human omega light chain protein 14.1 (Ig lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
	409653	AW451693	Hs.220826	ESTs	10.4
	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
15	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prola	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
	422406	AF025441	Hs.116206	Opa-interacting protein 5	10.3
20	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelat	10.3
	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [10.3
	448119	H38587	Hs.82295	dedicator of cyto-kinesis 1	10.2
	457288	AA521458	Hs.192738	ESTs	10.2
25	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
30	444514	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
	449501	AI652924	Hs.231942	ESTs	10.1
35	420731	AL042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159156	protocadherin 11	10.1
	400438	AF185611		Target	10.1
	438170	AI918685	Hs.184601	ESTs	10.1
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
40	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
	403038			Target Exon	10.0
	434674	AA831879	Hs.136985	ESTs	10.0
45	439885	AW56781	Hs.293837	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
	408392	U28831	Hs.44586	KIAA1641 protein	9.9
	421849	AW410872	Hs.106894	hypothetical protein FLJ20411	9.9
50	433384	AI021992	Hs.124244	ESTs	9.9
	443343	BE409809	Hs.301006	purine-rich element binding protein B	9.9
	437287	AW511443	Hs.258110	ESTs	9.9
	455978	AI310161	Hs.173524	ESTs	9.9
	435851	AA700946	Hs.191933	ESTs	9.9
55	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.9
	436869	AA595975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
	421602	AF111856	Hs.106039	solute carrier family 34 (sodium phosphate), member 2	9.8
60	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fls, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-080100-015-009 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
	442660	AW138174	Hs.130651	ESTs	9.8
65	436186	BE390717	Hs.5074	similar to S. pombe dm1	9.8
	426773	NM_015556	Hs.172180	KIAA0440 protein	9.8
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
	416347	AA216419		gb:nc18e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA clone si	9.7
	448752	AA593867	Hs.300842	KIAA1608 protein	9.7
70	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fls, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
	436523	BE612980	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00069 protein, partial cds	9.7
75	411930	F08485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100688	ESTs, Weakly similar to JE0350 Anterior gradient-2 (H	9.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [9.6
	409997	AI908065	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
	434957	AF283776	Hs.35380	x 001 protein	9.6
80	407292	AA876638		gb:nc45e08.s1 NCL_CGAP_Pr12 Homo sapiens cDNA clone s	9.6
	459108	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:nc51e10.s1 NCL_CGAP_Pr18 Homo sapiens cDNA clone s	9.6
	432074	AA525248	Hs.149723	ESTs	9.6
	440463	AI733087	Hs.129994	ESTs	9.6
	420861	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165893	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALIN (H-sap	9.6

	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA808106	Hs.123664	ESTs	9.6
5	417037	BE083936	Hs.80976	antigen identified by monoclonal antibody Ki-57	9.6
	449317	AW293413	Hs.132906	19A24 protein	9.6
	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374:gl 10764778[gb]AAG22817.1 AF302150_1 (AF30	9.5
10	414085	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1008851	9.5
	409802	AI337658	Hs.156351	ESTs	9.5
	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I76885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
15	418216	AA662240	Hs.283039	AF15q14 protein	9.5
	434573	AW372340	Hs.159717	ESTs	9.5
	439354	AF066174		gb:Homo sapiens full length insert cDNA clone Z894A08	9.5
	455410	AW936578		gb:PM2-DT0023-080300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400738			Target Exon	9.5
20	419474	AW958619	Hs.155849	ESTs	9.4
	406464			C17000168:gl 7294725[gb]AAF50062.1 (AE003644) CG7547	9.4
	407881	AW072003	Hs.40988	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
25	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423842	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
30	419988	W39388	Hs.55338	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
35	420897	AW139261	Hs.232280	ESTs	9.3
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI199810	Hs.267912	ESTs, Weakly similar to ALL7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein {	9.3
40	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
	428168	AA423849	Hs.79530	M5-14 protein	9.3
	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92862	Hs.35052	ESTs	9.3
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
45	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.3
	418606	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
	416009	C75253	Hs.220950	ESTs	9.3
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.126376	ESTs, Weakly similar to JC5314 CDC28cdc2-like kinase	9.2
50	417881	AI879117		gb:auS4g09.y1 Schmelder fetal brain 00004 Homo sapien	9.2
	446364	AW449650	Hs.202249	ESTs	9.2
	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA532644		gb:np87607.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI559308	Hs.24908	ESTs	9.2
55	457322	AB815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
	424317	AI885032	Hs.26017	ESTs	9.2
	433001	AF217513	Hs.278906	clone HQ0310 PRO0310p1	9.2
	404112	BE502729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
60	434960	AW374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	tRNA selenocysteine associated protein	9.1
	439158	R60323	Hs.183888	ESTs	9.1
	443081	H06858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
65	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFET LOCUS	9.1
	437044	AI035864	Hs.69517	cDNA for differentially expressed CO18 gene	9.1
	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89867	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgin-like 1	9.1
70	431405	AI470895	Hs.252674	ribosomal protein L10a	9.0
	405454			C12000541:gl 5729884[ref]NP_006539.1 IGF-1 mRNA-bln	9.0
	436362	AA806578	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
75	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125894	Hs.149306	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
	435074	AI760944	Hs.118937	ESTs	9.0
80	406722	H27488	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW283123	Hs.127554	ESTs	9.0
	431675	AA899985	Hs.202375	ESTs	9.0
	447184	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
5	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
	437866	AW891130	Hs.38173	ESTs	8.9
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	interferon-induced protein with tetratricopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
10	429228	AI553633	Hs.337139	ESTs	8.8
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EUROI	8.8
15	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AI146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191890	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
20	408805	H69912	Hs.48269	vaccinia related kinase 1	8.7
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410806	Hs.277973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
25	454132	AW131759	Hs.248286	ESTs	8.7
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.78078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441526	AW241867	Hs.127728	ESTs	8.7
30	459539	AI279186		gb:cm24a04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
	443148	AI034367	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
	424255	AI192657	Hs.143897	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038		gb:EST22383 Adipose tissue, white Hs Homo sapiens cDN	8.7
	443117	AI248826	Hs.42029	ESTs	8.6
	457434	AW626192	Hs.10851	hypothetical protein FLJ10875	8.6
35	442505	AW003775	Hs.198248	UDP-Gal4betaGlcNAc beta 1,4-galactosyltransferase, p	8.6
	430901	AA486833	Hs.126711	ESTs, Weakly similar to I38588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
40	415961	H10983	Hs.156919	ESTs	8.6
	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100606	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA458195	Hs.10056	hypothetical protein FLJ14621	8.6
45	458042	AW058464	Hs.6430	protein with polyglutamine repeat; cathepsin (cat) home	8.6
	456530	AL048437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.124814	ESTs	8.6
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
50	455161	BE145900		gb:MRU-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)	8.5
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	416018	U49395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C11001758:gc12621132ref1:MP_075243.1 MEGF1 [Rattus	8.5
55	438451	AI081972	Hs.220261	ESTs	8.5
	435176	AA744875	Hs.189413	ESTs	8.5
	443245	AI040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
60	403839			Target Exon	8.5
	434932	BE613162	Hs.284135	hypothetical protein MGC3036	8.5
	420991	AW504814	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE179190		gb:RC0-HT0813-210300-032-007 HT0813 Homo sapiens cDNA	8.4
65	402788			Target Exon	8.4
	423426	AW389579	Hs.128434	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110			NM_020245: Homo sapiens tubby super-family protein (T	8.4
70	424441	X14950	Hs.147097	H2A histone family, member X	8.4
	433155	AL037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
	414839	X03692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	8.4
	406867	AA157857	Hs.182265	keratin 19	8.4
	418278	AI088489	Hs.83937	hypothetical protein	8.4
75	458666	AW375333	Hs.199890	ESTs	8.4
	456248	AL035788	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19A24 protein	8.4
80	425891	AI041717	Hs.132141	ESTs	8.4
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587		gb:JL2-BT0731-240400-068-H04 BT0731 Homo sapiens cDNA	8.4
	426144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4